

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2005, 02:17:16 : Search time 59 Seconds

(without alignments)
1666.427 Million cell updates/sec

Title: US-10-245-013-48

Perfect score: 1036

Sequence: 1 MSPRTLPRPLSLGLSLCLC.....GTAEGGSGVASPAQAKDAEL 192

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1036	100.0	192	2	Q6UXS2
2	875	84.5	185	2	Q81XL7
3	793.5	76.6	186	2	Q8BU85
4	598	57.7	186	2	Q61Q80
5	427	41.2	137	1	MSRB_SALTI
6	427	41.2	137	1	MSRB_SALTY
7	423	40.8	202	2	Q9C8M2
8	420	40.5	147	2	Q8TT14
9	417	40.3	135	1	MSRB_STNEL
10	416	40.2	140	2	Q8PWF5
11	410.5	39.6	150	2	Q8IGS8
12	410.5	39.6	207	1	MSRB_DROME
13	408.5	39.4	153	2	Q8LAR2
14	408	39.4	137	2	Q83L66
15	407	39.3	151	1	MSRB_METTH
16	407	39.3	157	2	Q8IGC0
17	406	39.2	132	1	MSRB_PSEAE
18	405	39.1	137	1	MSRB_ECOLI
19	403	38.9	133	2	Q7ND97
20	400.5	38.7	143	2	Q63JM6
21	400.5	38.7	143	2	Q63V23
22	399	38.5	144	2	Q7V5H4
23	397.5	38.4	160	2	Q69XS8
24	396.5	38.3	137	1	MSRB_YERPE
25	396.5	38.3	137	2	Q66AP6
26	393	37.9	136	2	Q7N400
27	388	37.5	128	1	MSRB_RALSO
28	386	37.3	171	2	Q7QD74
29	384	37.1	166	2	Q72NN2
30	382.5	36.9	137	2	Q6BC90
31	382.5	36.9	175	2	Q6BC92

32	382	36.9	131	2	Q7U9C0
33	380.5	36.7	154	1	MSRB_VIBVU
34	380	36.7	175	2	Q86ES2
35	379.5	36.6	154	2	Q7MMC4
36	375.5	36.2	132	1	Q74B11
37	375	36.2	132	1	MSRB_LEPIN
38	373	36.0	139	2	Q6FAL8
39	373	36.0	175	2	Q78J03
40	372	35.9	133	2	Q7W5E3
41	372	35.9	133	2	Q7WCX8
42	370.5	35.8	137	2	Q86F85
43	370.5	35.8	147	1	MSRB_VIBPA
44	369	35.6	138	2	Q6N211
45	368	35.5	139	2	Q6D4P7
46	368	35.5	149	2	Q7NE61
47	367	35.4	133	2	Q7VTH6
48	366	35.3	142	2	Q6LNZ6
49	362	34.9	138	2	Q6MPT4
50	358	34.6	130	1	MSRB_PASMU
51	357	34.5	135	1	MSRB_AGR75
52	355	34.3	131	1	MSRB_PSRPK
53	355	34.3	139	1	MSRB_BRAJA
54	354	34.2	194	2	Q7UMT6
55	353.5	34.1	201	1	MSRB_HUMAN
56	351.5	33.9	147	1	MSRB_VIBCH
57	350	33.8	140	2	Q8MPC3
58	349	33.7	133	2	Q9HPZ3
59	348	33.6	135	1	MSB1_RHIME
60	347.5	33.5	139	2	Q6ADJ8
61	344	33.2	143	1	MSRB_BACHD
62	343	33.1	131	1	MSRB_PSESM
63	342.5	33.1	145	2	Q98Q62
64	342.5	33.1	165	2	Q6N2W1
65	342	33.0	164	2	Q8YQD2
66	340.5	32.9	319	2	Q67NJ7
67	340.5	32.9	356	1	MSAB_ACTAC
68	340	32.8	129	2	Q7NT50
69	340	32.8	157	1	MSRB_DEIRA
70	339.5	32.8	134	2	Q98F32
71	339	32.7	132	2	Q6SHV4
72	338	32.6	407	2	Q84FC0
73	337	32.5	134	2	Q73W66
74	337	32.5	143	2	Q72EK2
75	335	32.3	136	2	P71971
76	335	32.3	136	2	Q7TY50
77	333.5	32.2	180	2	Q6NW52
78	333.5	32.1	522	1	MSAB_NEIMA
79	332.5	32.1	522	1	MSAB_NEIMB
80	331.5	32.0	146	1	MSRB_CLOAB
81	331.5	32.0	185	2	Q8KG65
82	331	31.9	337	2	Q8GDS7
83	329	31.8	178	2	Q89HY4
84	329	31.8	317	2	Q73PT7
85	328.5	31.7	144	1	MSRB_LACPL
86	328.5	31.7	321	2	Q814J4
87	328.5	31.7	522	1	MSAB_NEIGO
88	325	31.4	135	2	Q82L08
89	325	31.4	390	2	Q7MFS9
90	324.5	31.3	145	1	MSRB_STRPY
91	324.5	31.3	164	2	Q7V3Q5
92	324.5	31.3	175	2	Q6MNN5
93	324.5	31.3	176	2	P72779
94	324.5	31.3	321	2	Q630G6
95	324.5	31.3	321	2	Q72X09
96	324.5	31.3	321	2	Q81JL7
97	324.5	31.3	321	2	Q6HAK1
98	324	31.3	135	2	Q9X828
99	324	31.3	380	2	Q8D3N9
100	323.5	31.2	145	1	MSRB_ENTRA
101	323	31.2	378	1	MSRB_VIBCH
102	322.5	31.1	145	1	MSRB_STRP3
103	322.5	31.1	199	2	Q6CUI4
104	322	31.1	153	2	Q6SG05

Q7U9C0	synechococ
Q8d849	vibrio vuln
Q86es2	schistosoma
Q7mmc4	vibrio vuln
Q74b11	geobacter s
Q8f7w8	leptospira
Q8fal8	acinetobact
Q78j03	mus musculu
Q7w5e3	bordetella
Q7wcx8	bordetella
Q86f85	schistosoma
Q8rme5	vibrio para
Q6n211	rhodopseudo
Q6d4p7	erwinia car
Q7ne61	gloeobacter
Q7vth6	bordetella
Q6lnz6	photobacter
Q6mpt4	bdellovibri
Q8cmb1	pasteurella
Q8ugx7	agrobacteri
Q88lq6	pseudomonas
Q89em9	bradyrhizob
Q7umy6	rhodospirall
Q9y3d2	homo sapien
Q8qkq0	vibrio chol
Q8mpc3	taenia soli
Q9hpz3	halobacteri
Q92ra4	rhizobium m
Q6adj8	leifsonia x
Q9cxd2	bacillus ha
Q885q1	pseudomonas
Q98q62	mycoplasma
Q6n2w1	rhodopseudo
Q8yqd2	anabaena sp
Q67nj7	symbiobacte
Q8a199	a peptide m
Q7nt50	chromobacte
Q9ruk6	deinococcus
Q98f32	rhizobium l
Q6shv4	uncultured
Q84fc0	myxococcus
Q73w66	mycobacteri
Q72ek2	desulfovibr
P71971	mycobacteri
Q7ty50	mycobacteri
Q6nw52	brachydanio
Q9jwm8	n peptide m
Q9kin8	n peptide m
Q97iu0	clostridium
Q8kg65	chlorobium
Q8gde7	heliobacill
Q83hy4	bradyrhizob
Q83pt7	treponema d
Q8w333	lactobacill
Q814j4	bacillus ce
P14930	n peptide m
Q82l08	streptomyce
Q7mf59	vibrio vuln
Q9zav6	streptococc
Q7vjq5	prochloroco
Q6mn95	bdellovibri
P72779	synechocyst
Q630g6	bacillus ce
Q72x09	bacillus ce
Q81j17	bacillus an
Q6nak1	bacillus th
Q9x828	streptomyce
Q8d3n9	vibrio vuln
Q9xb39	enterococcu
Q9klx6	v peptide m
Q8k7m6	streptococc
Q6cuy4	kluvaromyc
Q6sg05	uncultured

105	322	31.1	158	2	Q7R5S8	Q7r5e8	giardia lam	178	285	27.5	309	1	MSAB_STRPY	O99Yt1 s peptide m
106	322	31.1	159	1	MSRB_CAUCR	Q9a6b1	caulobacter	179	284.5	27.5	141	2	Q8LSP4	Q8leP4 arabadopsais
107	321	31.0	380	2	Q87JF1	Q87jfp1	vibrio para	180	284.5	27.5	143	2	O49707	O49707 arabadopsais
108	320.5	30.9	359	1	MSAB_HELPY	O25011	h peptide m	181	283	27.3	309	1	MSAB_STRP3	O938p0 s peptide m
109	318.5	30.7	147	1	MSB2_RHIME	Q92V46	rhizobium m	182	281.5	27.2	127	2	O9C1Z7	O9c1Z7 pichia past
110	318.5	30.7	359	1	MSAB_HELPJ	Q92mk8	h peptide m	183	281.5	27.2	139	2	O9ZS91	O9zS91 arabadopsais
111	317.5	30.6	145	1	MSRB_STRP8	Q9p172	streptococc	184	281.5	27.2	164	2	O7NB05	O7nb05 mycoplasma
112	317.5	30.6	187	2	Q7P348	Q7p348	fusobacteri	185	278.5	26.9	141	2	O9M0Z4	O9m0Z4 arabadopsais
113	316.5	30.6	167	2	Q98D81	Q98d81	rhizobium l	186	278.5	26.9	153	2	O8GMF4	O8gmF4 arabadopsais
114	316.5	30.6	473	2	Q8R5X2	Q8r5x2	rhizobacteri	187	278	26.8	53	2	O6MZU8	O6mZu8 homo sapien
115	315	30.4	147	2	Q6W178	Q6w178	rhizobium s	188	277.5	26.8	150	1	MSRB_MYCGE	P47686 mycoplasma
116	314.5	30.4	143	1	MSRB_BACSU	P54155	bacillus su	189	277	26.7	155	2	O6AG95	O6ag95 leifsonia x
117	314	30.3	319	2	Q8EQG6	Q8eqg6	oceanobacil	190	276.5	26.7	155	1	MSRB_XYLFA	O9pf29 xylella fas
118	313.5	30.3	353	1	MSAB_HAEIN	P45213	h peptide m	191	274.5	26.5	141	2	O49706	O49706 arabadopsais
119	312.5	30.2	337	1	MSAB_CAMPE	Q93kf3	c peptide m	192	274.5	26.5	144	2	O8VI86	O8vY86 arabadopsais
120	311.5	30.1	168	2	Q7V9D4	Q7v9d4	prochloroco	193	274.5	26.5	155	1	MSRB_CLOPE	Q87aJ9 xylella fas
121	311	30.0	130	2	Q7VLV8	Q7vLv8	haemophilus	194	273.5	26.4	147	1	MSRB_CLOPE	O8xjZ6 clostridium
122	311	30.0	148	2	Q9KSM0	Q9ksm0	vibrio chol	195	273	26.4	142	1	MSRB_LACLA	O9CjJ7 lactococcus
123	310.5	30.0	144	2	Q8E026	Q8e026	streptococc	196	271.5	26.2	229	2	O6AUK5	O6auK5 oryza sativ
124	310.5	30.0	144	2	Q8E026	Q8e026	streptococc	197	271	26.2	221	1	MSAB_TREPA	O83641 t peptide m
125	310	29.9	366	2	Q6ANW8	Q6anw8	desulfotale	198	268	25.9	327	2	O8G6S0	O8g6S0 bifidobacte
126	307.5	29.7	146	2	Q6KI58	Q6ki58	mycoplasma	199	264.5	25.5	129	2	O6CCY5	O6ccY5 yarrowia li
127	307	29.6	151	2	Q65ID2	Q65id2	bacillus li	200	264.5	25.5	445	2	O82U12	O82u12 nitrosomona
128	305.5	29.5	202	2	Q8LE28	Q8le28	arabadopsais	201	264	25.5	146	2	O751W7	O751W7 ashbya goss
129	305.5	29.5	202	2	Q8C5C8	Q8c5c8	arabadopsais	202	263	25.4	168	1	YCD3_YEAST	P25566 saccharomyc
130	304	29.3	136	2	Q8NFB6	Q8nfb6	corynebacte	203	262	25.3	284	2	O83C28	Q83c28 coxiella bu
131	303.5	29.3	142	1	MSRB_STARP	Q8csk6	staphylococ	204	261.5	25.2	155	2	O9ZS90	Q9zS90 arabadopsais
132	303.5	29.3	163	2	Q6X965	Q6x965	staphylococ	205	259	25.0	309	2	O6MSJ8	O6mSj8 mycoplasma
133	303.5	29.3	298	2	Q8RG79	Q8rgt9	fusobacteri	206	255.5	24.7	224	2	O48984	O48984 mycoplasma
134	303.5	29.3	352	2	O7MT91	Q7mt91	porphyronon	207	253	24.4	301	2	O8E802	O8ee02 shewanella
135	302.5	29.2	311	1	MAB2_STRPN	P65443	s peptide m	208	247.5	23.9	139	2	O9M0Z5	O9m0Z5 arabadopsais
136	302.5	29.2	311	1	MAB2_STRR6	P65444	s peptide m	209	243	23.5	284	2	O6MCL1	O6mcL1 parachlamyd
137	302	29.2	154	2	Q8P4Q6	Q8p4q6	xanthomonas	210	235.5	22.7	282	2	O7UW48	Q7uW48 rhodopirell
138	302	29.2	154	2	Q8P4Q6	Q8p4q6	xanthomonas	211	233	22.5	119	2	O9PN12	O9pn12 campylobact
139	301.5	29.1	361	2	Q64QB5	Q64qb5	bacteroides	212	228.5	22.1	122	2	O7VGA6	O7vGa6 helicobacte
140	301	29.1	151	2	O68E43	Q68e43	aeromonas p	213	214	20.7	124	2	O49708	O49708 arabadopsais
141	301	29.1	162	2	Q7RZD6	Q7rzd6	neurospora	214	207.5	20.0	116	1	MSRX_HUMAN	O9nzv6 homo sapien
142	300	29.0	159	1	MSRB_CLOHI	Q9znj9	clostridium	215	207.5	20.0	116	2	O96RX6	O96rx6 homo sapien
143	300	29.0	281	2	Q2ZS93	Q9zS93	arabadopsais	216	192.5	18.6	116	1	MSRX_MOUSE	Q9jlC3 mus musculo
144	299	28.9	166	2	Q7VEJ8	Q7vej8	prochloroco	217	183.5	17.7	110	2	O6NWX6	O6nWx6 brachydano
145	299	28.9	284	2	Q8KCX9	Q8kcX9	chlorobium	218	183.5	17.7	110	2	O802G6	O802G6 brachydano
146	298.5	28.8	294	2	O7P464	Q7p464	fusobacteri	219	180.5	17.4	93	2	O6TXU6	O6txU6 brassica ra
147	298	28.8	136	2	Q9M0Z6	Q9m0Z6	arabadopsais	220	155	15.0	92	2	O66HU0	O66hu0 brachydano
148	297.5	28.7	152	1	YL56_CAEEL	P34436	caenorhabdi	221	144.5	13.9	92	2	O66DIP7	O66dI7 xenopus tro
149	297.5	28.7	168	2	Q7UAB1	Q7uaB1	synechococc	222	120	11.6	1133	2	O8I949	Q8i949 anopheles g
150	296.5	28.6	342	2	Q8A4U8	Q8a4u8	bacteroides	223	115	11.1	283	2	O8GLG5	O8glG5 streptococc
151	295.5	28.5	164	2	Q92SF8	Q92sf8	rhizobium m	224	106.5	10.3	76	2	O6P6Y5	O6p6Y5 brachydano
152	294.5	28.4	136	2	Q8NGV7	O8ngv7	corynebacte	225	98	9.5	241	2	O7PGE2	O7pGg2 anopheles g
153	293	28.3	146	1	MSRB_BRUME	P65447	brucella me	226	94.5	9.1	539	2	O66J41	O66j41 xenopus lae
154	293	28.3	146	1	MSRB_BRUSU	P65448	brucella su	227	94	9.1	445	2	O9T281	O9tZ81 caenorhabdi
155	292	28.2	143	2	Q8LCW5	Q8lcw5	arabadopsais	228	90.5	8.7	127	2	O6RF46	O6rf46 arabadopsais
156	292	28.2	143	2	Q84JT6	Q84jt6	arabadopsais	229	89	8.6	474	2	O9AJJ2	O9aJj2 marine cfb-
157	292	28.2	168	2	Q84PAL	Q84pal	oryza sativ	230	89	8.6	2496	1	HORN_MOUSE	Q9vH88 drosophila
158	291	28.1	151	1	MSRB_MYCPN	P75129	mycoplasma	231	89	8.6	2885	1	Q9VH88	Q9vH88 drosophila
159	290.5	28.0	145	2	O71YF7	Q71yf7	listeria mo	232	89	8.6	2895	1	HYD_DROME	P51592 drosophila
160	290.5	28.0	163	2	Q6FX89	Q6fx89	candida gla	233	88.5	8.5	474	2	O9AJK0	O9aJk0 marine cfb-
161	290	28.0	137	2	Q8FPI7	Q8fpI7	corynebacte	234	88	8.5	197	2	O65IH1	O65iH1 bacillus li
162	289.5	27.9	143	1	MSRB_LISMO	Q9y641	listeria mo	235	88	8.5	474	2	O9AJL1	O9aJl1 marine cfb-
163	288.5	27.8	129	2	Q6BXR0	Q6bxr0	debaryomyce	236	87.5	8.4	1178	2	O8CB68	O8cb68 mus musculo
164	287.5	27.8	142	1	MSRB_STAAN	P65451	staphylococ	237	87	8.4	196	2	O8G0J9	O8g0J9 brucella su
165	287.5	27.8	142	1	MSRB_STAAN	P99065	staphylococ	238	86.5	8.3	961	2	O93WZ8	O93wZ8 phaseolus v
166	287.5	27.8	142	1	MSRB_STAAN	Q93p62	staphylococ	239	86	8.3	108	2	O742B5	O742B5 mycobacteri
167	287.5	27.8	142	2	Q6G9D8	Q6g9d8	staphylococ	240	86	8.3	108	2	O9AJJ5	O9aJj5 marine cfb-
168	287.5	27.8	142	2	Q6GGY4	Q6ggy4	staphylococ	241	86	8.3	474	2	O9AJK3	O9aJk3 marine cfb-
169	286.5	27.7	170	1	MSRB_LISIN	Q92ae9	listeria in	242	84.5	8.2	234	2	O7PQC5	O7pJc5 anopheles g
170	286	27.6	140	2	Q7MC54	Q7mc54	vibrio vuln	243	84.5	8.2	293	2	O7PQC5	O7pJc5 anopheles g
171	286	27.6	199	2	Q8D587	Q8d587	vibrio vuln	244	84.5	8.2	303	2	O7PRD0	O7prD0 anopheles g
172	286	27.6	311	1	MSAB_STRGC	Q9lam9	s peptide m	245	84.5	8.2	556	2	O9GSE0	O9gSs0 drosophila
173	285.5	27.6	142	2	Q74IX6	Q74ix6	lactobacill	246	84.5	8.2	556	2	O9VIX3	O9vix3 drosophila
174	285.5	27.6	148	2	Q6A8V0	Q6a8v0	propionibac	247	84.5	8.2	557	2	O8INW7	O8inW7 drosophila
175	285.5	27.6	312	1	MAB1_STRPN	P35593	s peptide m	248	84.5	8.2	557	2	O8MQX3	O8mqX3 drosophila
176	285	27.5	138	2	O9Y7K1	Q9y7k1	schizosacch	249	84.5	8.2	581	2	O9BFP9	O9bP9 drosophila
177	285	27.5	309	1	MSAB_STRP8	Q9p046	s peptide m	250	84.5	8.2	581	2	O9VIX2	O9vix2 drosophila

251	84.5	8.2	688	2	Q7SCC4	Q7sc4	neurospora	324	77	7.4	820	2	Q6NN10	Q6nn10	drosophila
252	84.5	8.2	753	2	Q86Z16	Q86zi6	neurospora	325	77	7.4	826	2	Q9Y094	Q9y094	drosophila
253	84.5	8.2	2194	1	GLSN_WEDSA	Q03460	medicago sa	326	77	7.4	820	2	Q9LV03	Q9lv03	arabidopsis
254	84.5	8.2	2194	1	GLSN_WEDSA	Q40360	medicago sa	327	76.5	7.4	450	1	DGT1_STRAW	Dgt1	streptomyces
255	84	8.1	134	2	Q7WB24	Q7wb24	bordetella	328	76.5	7.4	609	2	G61618	G61618	oryza sativa
256	84	8.1	134	2	Q7WB24	Q7wb24	bordetella	329	76.5	7.4	897	1	SYI_FERPE	SYI_FERPE	ferrobact
257	84	8.1	474	2	Q9AJI8	Q9aji8	marine cfb-	330	76.5	7.4	1028	2	Q9JLLO	Q9jllo	mus musculus
258	84	8.1	474	2	Q9AJI8	Q9aji8	marine cfb-	331	76.5	7.4	2638	2	Q30914	Q30914	streptomyces
259	84	8.1	474	2	Q9FAW3	Q9faw3	marine bact	332	76	7.3	313	2	Q74M60	Q74m60	nanoarchaea
260	83.5	8.1	325	2	Q6WA15	Q6wa15	parachlamydia	333	76	7.3	350	2	Q7R6M8	Q7r6m8	giardia lam
261	83.5	8.1	1366	2	Q6CI34	Q6ci34	yellowia li	334	76	7.3	376	2	Q811V5	Q811v5	plasmodium
262	83	8.0	193	2	Q6P2T6	Q6p2t6	brachydanio	335	76	7.3	391	2	Q8RR05	Q8rr05	cytophaga s
263	83	8.0	1740	2	Q811P8	Q811p8	mus musculus	336	76	7.3	642	2	Q8MPM6	Q8mpm6	giardia lam
264	82.5	8.0	197	2	Q966T5	Q966t5	drosophila	337	76	7.3	893	2	Q93V06	Q93v06	eubacterium
265	82.5	8.0	255	2	Q81NW6	Q81nw6	drosophila	338	76	7.3	1184	1	BIMC_EMENI	Bimc	emericella
266	82.5	8.0	699	2	Q9U2U1	Q9u2u1	caenorhabditis	339	75.5	7.3	288	2	Q8BLF6	Q8blf6	mus musculus
267	82	7.9	151	2	Q91RD9	Q91rd9	tt virus	340	75.5	7.3	434	2	Q22291	Q22291	arabidopsis
268	82	7.9	411	1	IH_HUMAN	Q14623	homo sapiens	341	75.5	7.3	509	2	Q7FN94	Q7fn94	anopheles g
269	82	7.9	474	2	Q9AJJ7	Q9ajj7	marine cfb-	342	75.5	7.3	548	2	Q7S6Y2	Q7s6y2	neurospora
270	82	7.9	474	2	Q9AJK1	Q9ajk1	marine cfb-	343	75.5	7.3	549	2	Q8CIG1	Q8cig1	mus musculus
271	82	7.9	685	2	Q7QWD9	Q7qwd9	giardia lam	344	75.5	7.3	550	2	Q8R1D1	Q8r1d1	mus musculus
272	81.5	7.9	550	2	Q81N11	Q81n11	drosophila	345	75.5	7.3	645	2	Q9P282	Q9p282	homo sapiens
273	81.5	7.9	625	2	Q81GX9	Q81gx9	drosophila	346	75.5	7.3	1174	2	Q9N8S0	Q9n8s0	trypanosoma
274	81.5	7.9	625	2	Q8MSQ3	Q8msq3	drosophila	347	75	7.2	332	2	Q925Q2	Q925q2	mus musculus
275	81.5	7.9	712	2	Q81GX5	Q81gx5	drosophila	348	75	7.2	374	2	Q6ZNI1	Q6zni1	homo sapiens
276	81.5	7.9	712	2	Q9VG15	Q9vg15	drosophila	349	75	7.2	408	2	Q8J2S3	Q8j2s3	hericium er
277	81	7.8	251	2	Q9VPF2	Q9vpf2	drosophila	350	75	7.2	460	2	Q8GTP8	Q8gtp8	pyrus commu
278	81	7.8	312	2	Q7VM88	Q7vm88	haemophilus	351	75	7.2	467	2	Q66R29	Q66r29	oikopleura
279	81	7.8	317	2	Q9L7Q3	Q9l7q3	haemophilus	352	75	7.2	474	2	Q9AJK5	Q9ajk5	marine cfb-
280	81	7.8	368	2	Q73XT1	Q73xt1	mycobacterium	353	75	7.2	474	2	Q9AJK7	Q9ajk7	marine cfb-
281	81	7.8	498	2	Q6PY44	Q6py44	brachydanio	354	74.5	7.2	72	2	Q9CHL4	Q9chl4	lactococcus
282	81	7.8	556	2	Q9PFK3	Q9pfk3	arabidopsis	355	74.5	7.2	206	2	Q94H15	Q94h15	rat
283	81	7.8	562	1	CD6_MOUSE	Q89033	mus musculus	356	74.5	7.2	206	2	Q7XGS8	Q7xgs8	oryza sativa
284	80.5	7.8	446	2	Q8W0E9	Q8w0e9	oryza sativa	357	74.5	7.2	391	2	Q8RR06	Q8rr06	cytophaga s
285	80.5	7.8	814	2	Q62WJ8	Q62wj8	homo sapiens	358	74.5	7.2	396	2	Q641P2	Q641p2	xenopus lae
286	79.5	7.7	128	2	Q812Q2	Q812q2	plasmodium	359	74.5	7.2	539	2	Q7R5G1	Q7r5g1	giardia lam
287	79.5	7.7	561	2	Q6RUG6	Q6rug6	cricketul	360	74.5	7.2	591	2	Q810C3	Q810c3	rat
288	79.5	7.7	1043	1	SVI_METH	Q27428	methanobact	361	74.5	7.2	840	2	Q810C5	Q810c5	rat
289	79	7.6	320	2	Q7QAM3	Q7qam3	anopheles g	362	74.5	7.2	1050	2	Q810C5	Q810c5	rat
290	79	7.6	427	2	Q6S791	Q6s791	bovine vira	363	74.5	7.2	1065	1	KDGI_HUMAN	Kdgi	homo sapiens
291	79	7.6	478	2	Q9H5P0	Q9h5p0	homo sapiens	364	74.5	7.2	1105	2	Q9JME3	Q9jme3	rat
292	79	7.6	510	2	Q96HQ0	Q96hq0	homo sapiens	365	74.5	7.2	1335	2	Q7RLM3	Q7rlm3	giardia lam
293	79	7.6	549	2	Q8C635	Q8c635	mus musculus	366	74	7.1	227	1	ZN77_HUMAN	Zn77	homo sapiens
294	79	7.6	782	2	Q6GQR6	Q6gqr6	mus musculus	367	74	7.1	238	2	Q8PNN3	Q8pnn3	xanthomonas
295	79	7.6	1023	2	Q9JIC3	Q9jic3	mus musculus	368	74	7.1	239	1	CWP1_YEAST	Cwp1	saccharomyc
296	78.5	7.6	273	2	Q6S150	Q6s150	nicotiana t	369	74	7.1	271	1	Y398_METUA	Y398	methanococ
297	78.5	7.6	322	2	Q6S151	Q6s151	arabidopsis	370	74	7.1	306	2	Q65X09	Q65x09	oryza sativa
298	78.5	7.6	458	2	Q7M6X8	Q7m6x8	mus musculus	371	74	7.1	315	2	Q97601	Q97601	oryctolagus
299	78.5	7.6	1100	2	Q57576	Q57576	cynops pyr	372	74	7.1	349	2	Q8DU36	Q8du36	streptococ
300	78.5	7.6	1121	2	Q72FF8	Q72ff8	desulfovibr	373	74	7.1	372	2	Q9YK09	Q9yk09	bovine vira
301	78	7.5	274	2	Q40897	Q40897	petunia hyb	374	74	7.1	391	2	Q8RQX9	Q8rx9	cytophaga s
302	78	7.5	448	2	Q7KPF42	Q7kpf42	drosophila	375	74	7.1	391	2	Q8RQZ8	Q8rz8	cytophaga s
303	78	7.5	509	2	Q87715	Q87715	acidianus b	376	74	7.1	401	2	Q9PRG7	Q9prg7	xenopus lae
304	78	7.5	561	2	Q699V2	Q699v2	chimpanzee	377	74	7.1	420	2	Q9PSM1	Q9psm1	xenopus lae
305	78	7.5	798	2	Q9VFN8	Q9vfn8	drosophila	378	74	7.1	474	2	Q9AJK9	Q9ajk9	cytophaga s
306	78	7.5	948	2	Q8E225	Q8e225	leptospira	379	74	7.1	474	2	Q9AJLO	Q9ajlo	cytophaga s
307	77.5	7.5	169	2	Q8NQ05	Q8nq05	corynebacte	380	74	7.1	474	2	Q9PAV1	Q9pav1	mus musculus
308	77.5	7.5	280	2	Q6M4X0	Q6m4x0	corynebacte	381	74	7.1	524	1	GLPK_MOUSE	Glpk	ectocarpus
309	77.5	7.5	358	2	Q9KEM8	Q9kbw8	bacillus ha	382	74	7.1	547	2	Q8ONE4	Q8c2m1	mus musculus
310	77.5	7.5	446	2	Q79825	P79825	oncorhynch	383	74	7.1	553	2	Q8C2M1	Q8c8x0	mus musculus
311	77.5	7.5	948	2	Q72MG7	Q72mg7	leptospira	384	74	7.1	559	2	Q8C8X0	Q8c8x0	mus musculus
312	77.5	7.5	1044	1	SVI_METH	P26499	methanobact	385	74	7.1	660	2	Q7Q458	Q7q458	anopheles g
313	77	7.4	134	2	Q7VF51	Q7vy51	bordetella	386	74	7.1	708	2	Q7QUX3	Q7qux3	giardia lam
314	77	7.4	208	2	Q9NDR6	Q9ndr6	branchiosto	387	74	7.1	709	2	Q9XTJ7	Q9xtj7	giardia lam
315	77	7.4	443	2	Q9N9T0	Q9n9t0	leishmania	388	74	7.1	710	1	TOP1_LACIA	Top1	lactococcus
316	77	7.4	484	2	Q64HY3	Q64hy3	mus musculus	389	74	7.1	751	2	Q74ZL3	Q74z13	ashbya gos
317	77	7.4	545	2	Q86XJ3	Q86xj3	homo sapiens	390	74	7.1	838	2	Q6NSM6	Q6nsm6	brachydanio
318	77	7.4	549	2	Q9WU64	Q9wu64	mus musculus	391	74	7.1	922	2	Q94GK6	Q94gk6	oryza sativa
319	77	7.4	611	1	CAP3_ARATH	Q8gx47	arabidopsis	392	74	7.1	1515	2	Q7PSW4	Q7psw4	anopheles g
320	77	7.4	611	2	Q7OWS7	Q7uws7	rhodospirell	393	74	7.1	1712	1	LTBI_RAT	Q0918	rat
321	77	7.4	663	2	Q16057	O16057	drosophila	394	74	7.1	1712	1	LTBI_RAT	Q0918	rat
322	77	7.4	679	2	Q8A2E0	Q8a2e0	bacteroides	395	74	7.1	2322	2	Q9DYD4	Q9dyd4	rabbit
323	77	7.4	739	2	Q9GS24	Q9gs24	giardia lam	396	74	7.1	2344	1	POLN_RHDV	P27410	r non-struc

397	74	7.1	2344	2	Q6QWJ0	Q6qwj0 rabbit hemo	470	72	6.9	230	2	Q8LC78	Q8lc78 arabidopsis
398	74	7.1	2344	2	Q86114	Q86114 rabbit hemo	471	72	6.9	230	2	Q8LFX9	Q8lfx9 arabidopsis
399	74	7.1	2344	2	Q86119	Q86119 rabbit hemo	472	72	6.9	247	2	P71851	P71851 mycobacteri
400	74	7.1	2344	2	Q89273	Q89273 rabbit hemo	473	72	6.9	247	2	Q7TW83	Q7tw83 mycobacteri
401	74	7.1	2344	2	Q8EMC2	Q8emc2 rabbit hemo	474	72	6.9	264	2	Q8L602	Q8l602 arabidopsis
402	74	7.1	3224	1	R8P2 HUMAN	P49792 homo sapien	475	72	6.9	273	2	Q672J1	Q672j1 homo sapien
403	74	7.1	3897	2	Q8Y117	Q6y117 bovine vira	476	72	6.9	291	1	NAK1 ECOL6	Q8fd60 escherichia
404	73.5	7.1	94	2	Q8XHB5	Q8xhb5 clostridium	477	72	6.9	294	2	Q8LC79	Q8lc79 arabidopsis
405	73.5	7.1	168	2	Q7RHV5	Q7rhv5 plasmodium	478	72	6.9	333	2	Q9S849	Q9s849 arabidopsis
406	73.5	7.1	176	2	Q93ZD8	Q93zd8 arabidopsis	479	72	6.9	339	2	Q24693	Q24693 dugesia tig
407	73.5	7.1	223	2	Q9HFH0	Q9hfh0 penicillium	480	72	6.9	339	2	Q24701	Q24701 dugesia tig
408	73.5	7.1	363	2	Q6CL86	Q6cl86 kluyveromyc	481	72	6.9	346	2	Q9HXL6	Q9hxl6 pseudomonas
409	73.5	7.1	367	2	Q96GES	Q96ges homo sapien	482	72	6.9	370	2	Q9Z9V6	Q9z9v6 bacillus ha
410	73.5	7.1	395	2	Q66IG4	Q66ig4 xenopus tro	483	72	6.9	372	2	Q9YK07	Q9yk07 bovine vira
411	73.5	7.1	396	2	Q7ZMW3	Q7zwm3 xenopus lae	484	72	6.9	386	2	Q65793	Q65793 bovine vira
412	73.5	7.1	406	2	Q7RLH9	Q7rlh9 giardia lam	485	72	6.9	400	2	Q9KGA7	Q9kga7 bacillus ha
413	73.5	7.1	414	2	Q8BI23	Q8bi23 mus musculu	486	72	6.9	422	2	Q20082	Q20082 caenorhabdi
414	73.5	7.1	521	2	Q7RZ86	Q7rz86 neurospora	487	72	6.9	427	2	Q65794	Q65794 bovine vira
415	73.5	7.1	559	2	Q9Y2P0	Q9y2p0 homo sapien	488	72	6.9	441	2	Q96DL8	Q96dl8 homo sapien
416	73.5	7.1	604	2	Q7R5F1	Q7r5f1 giardia lam	489	72	6.9	442	2	Q6PK81	Q6pk81 homo sapien
417	73.5	7.1	683	2	Q960I3	Q960i3 drosophila	490	72	6.9	454	2	Q64HW0	Q64hw0 trichoderma
418	73.5	7.1	705	2	Q04310	O04310 arabidopsis	491	72	6.9	460	2	Q6DD07	Q6dd07 xenopus lae
419	73.5	7.1	1104	2	Q8BHQ4	Q8bhq4 mus musculu	492	72	6.9	484	2	Q86V01	Q86v01 homo sapien
420	73.5	7.1	1541	2	Q6ZQE2	Q6zqe2 mus musculu	493	72	6.9	529	1	Z490 HUMAN	Q9ulm2 homo sapien
421	73.5	7.1	1560	2	Q8H5I5	Q8h5i5 oryza sativ	494	72	6.9	629	2	Q9UI92	Q9ui92 homo sapien
422	73.5	7.1	1788	2	Q6NV66	Q6nv66 mus musculu	495	72	6.9	647	2	Q96031	Q96031 homo sapien
423	73.5	7.1	2653	2	Q25253	Q25253 lucilia cup	496	72	6.9	685	2	Q7Q9N6	Q7q9n6 anopheles g
424	73	7.0	121	2	Q7PYW6	Q7pyw6 anopheles g	497	72	6.9	714	2	Q9NYW8	Q9nyw8 homo sapien
425	73	7.0	152	2	Q6I5J1	Q6i5j1 oryza sativ	498	72	6.9	824	2	Q72GB7	Q72gb7 thermus the
426	73	7.0	168	2	Q8BTA4	Q8bta4 homo sapien	499	72	6.9	1053	2	Q9VC20	Q9vc20 drosophila
427	73	7.0	192	1	C8R1 HUMAN	P21291 homo sapien	500	72	6.9	1113	2	Q9VC19	Q9vc19 drosophila
428	73	7.0	199	2	Q94476	Q94476 dictyosteli	501	72	6.9	1365	2	Q96Q28	Q96q28 homo sapien
429	73	7.0	202	2	Q8MML4	Q8mml4 dictyosteli	502	72	6.9	3913	2	Q8JRK3	Q8jrk3 bovine vira
430	73	7.0	230	1	RNS1 ARATH	P42813 arabidopsis	503	72	6.9	3913	2	Q6Y116	Q6y116 bovine vira
431	73	7.0	387	2	Q86BC8	Q86bc8 drosophila	504	72	6.9	3913	2	Q9WP30	Q9wp30 bovine vira
432	73	7.0	411	1	1FH MOUSE	P97812 mus musculu	505	71.5	6.9	145	2	Q9SYL5	Q9sy15 arabidopsis
433	73	7.0	449	2	Q80X19	Q80xi9 mus musculu	506	71.5	6.9	188	2	Q6CBQ9	Q6cbq9 varrowia li
434	73	7.0	478	2	Q788Q7	Q788q7 xenopus lae	507	71.5	6.9	242	2	Q8T0V6	Q8t0v6 drosophila
435	73	7.0	493	2	Q88701	Q88701 xenopus lae	508	71.5	6.9	265	2	Q758N0	Q758n0 ashyia goss
436	73	7.0	559	1	PAXI CHICK	P49024 gallus gall	509	71.5	6.9	304	2	Q75K48	Q75k48 oryza sativ
437	73	7.0	597	2	Q6SIF1	Q6sif1 emericella	510	71.5	6.9	343	2	Q74BP5	Q74bp5 geobacter s
438	73	7.0	611	2	Q6CAD5	Q6cad5 varrowia li	511	71.5	6.9	351	2	Q65SX1	Q65sx1 manheimia
439	73	7.0	711	2	Q74AY3	Q74ay3 geobacter s	512	71.5	6.9	353	2	Q7Z783	Q7z783 homo sapien
440	73	7.0	851	2	Q69ZT8	Q69zt8 mus musculu	513	71.5	6.9	359	2	Q9QWF8	Q9qwf8 mus musculu
441	73	7.0	1160	2	Q9WP28	Q9wp28 bovine vira	514	71.5	6.9	376	2	Q98DD2	Q98dd2 rhizobium l
442	73	7.0	1244	1	SLA1 YEAST	P32790 saccharomyc	515	71.5	6.9	387	2	Q9QWF9	Q9qwf9 mus musculu
443	73	7.0	2399	2	Q9ZKS9	Q9zks9 helicobacte	516	71.5	6.9	391	2	Q8RQY1	Q8rqy1 cytophaga s
444	72.5	7.0	123	2	Q80PV0	Q80pv0 porcine rep	517	71.5	6.9	391	2	Q8RQY2	Q8rqy2 cytophaga s
445	72.5	7.0	157	2	Q8NFU0	Q8nfu0 corynebacte	518	71.5	6.9	449	2	Q7NMW8	Q7nmw8 chromobacte
446	72.5	7.0	195	2	Q6AJQ7	Q6ajq7 desulfotale	519	71.5	6.9	450	2	Q8G555	Q8g555 bifidobacte
447	72.5	7.0	201	2	Q9RC72	Q9rc72 bacillus ha	520	71.5	6.9	453	2	Q81ZA6	Q81za6 mus musculu
448	72.5	7.0	248	2	Q9HHZ0	Q9hhz0 halobacteri	521	71.5	6.9	474	2	Q9FAV6	Q9fav6 cytophaga m
449	72.5	7.0	329	2	Q9ANU0	Q9anu0 streptomyce	522	71.5	6.9	540	1	Z136 HUMAN	P52737 homo sapien
450	72.5	7.0	331	2	Q6AY81	Q6ay81 rattus norv	523	71.5	6.9	541	1	GF11 DROME	Q9n658 drosophila
451	72.5	7.0	347	2	Q6ZAJ6	Q6zaj6 oryza sativ	524	71.5	6.9	638	2	Q8NBH6	Q8nbh6 homo sapien
452	72.5	7.0	401	2	Q9U3U1	Q9u3ul caenorhabdi	525	71.5	6.9	698	2	Q7NBR4	Q7nbr4 mycoplasma
453	72.5	7.0	453	1	TMS3 MOUSE	Q8kit0 mus musculu	526	71.5	6.9	703	1	FELL1 HUMAN	P23142 homo sapien
454	72.5	7.0	474	1	Y891 MYCPN	P75295 mycoplasma	527	71.5	6.9	707	2	Q7NAN8	Q7nan8 mycoplasma
455	72.5	7.0	495	2	Q9KCA5	Q9kc45 bacillus ha	528	71.5	6.9	744	1	Z483 HUMAN	Q8tf39 homo sapien
456	72.5	7.0	602	2	Q9VUL3	Q9vul3 drosophila	529	71.5	6.9	749	2	Q8BOD7	Q8b0d7 mus musculu
457	72.5	7.0	671	1	Z443 HUMAN	Q9y2a4 homo sapien	530	71.5	6.9	820	2	Q9FFK8	Q9ffk8 arabidopsis
458	72.5	7.0	688	2	O44633	O44633 caenorhabdi	531	71.5	6.9	904	2	O6NZE0	O6nzo0 mus musculu
459	72.5	7.0	752	2	Q88MB3	Q88mb3 pseudomonas	532	71.5	6.9	982	2	Q8VID5	Q8vid5 mus musculu
460	72.5	7.0	836	2	Q86UE3	Q86ue3 homo sapien	533	71.5	6.9	983	2	Q7NFW5	Q7nfw5 gloeobacter
461	72.5	7.0	854	2	Q9F2P0	Q9f2p0 streptomyce	534	71.5	6.9	1024	2	O6L206	O6l206 picophyllus
462	72.5	7.0	866	2	O6FPF8	O6fpf8 candida gla	535	71.5	6.9	1042	2	Q8Z5Y8	Q8z5y8 salmomella
463	72.5	7.0	990	2	O74202	O74202 emericella	536	71.5	6.9	1091	1	NCAL CHICK	P13590 gallus gall
464	72.5	7.0	1115	1	NCAL MOUSE	P13595 mus musculu	537	71.5	6.9	1286	2	Q7ZYF0	Q7zyf0 xenopus lae
465	72.5	7.0	1476	2	Q93EP6	Q93ep6 photorhabdu	538	71.5	6.9	1312	2	O15090	O15090 homo sapien
466	72.5	7.0	1519	2	Q8WPN0	Q8wpn0 oikopleura	539	71.5	6.9	1359	2	Q9NKQ3	Q9nkq3 leishmania
467	72.5	7.0	1791	2	Q7EPZL0	Q7epz10 anopheles g	540	71.5	6.9	1406	2	Q9W6V5	Q9w6v5 gallus gall
468	72	6.9	176	2	Q8YHB5	Q8yhb5 bruceella me	541	71.5	6.9	2157	2	Q8LHF0	Q8lhf0 oryza sativ
469	72	6.9	197	2	Q9VYMO	Q9vymo drosophila	542	71.5	6.9	2166	2	Q9ZNX7	Q9znx7 oryza sativ

543	71.5	6.9	2711	2	Q6X0P1	Q6x0p1 glycine max	616	70.5	6.8	359	2	Q8N988	Q8n988 homo sapien
544	71.5	6.9	3897	2	Q09461	Q09461 border dise	617	70.5	6.8	364	2	Q7T265	Q7t265 xenopus tro
545	71	6.9	173	2	Q7VBD1	Q7vbd1 prochloroco	618	70.5	6.8	373	2	Q8W524	Q8w524 bacterioph
546	71	6.9	174	2	Q7V7E7	Q7v7e7 prochloroco	619	70.5	6.8	412	2	Q70DX1	Q70dx1 streptomyce
547	71	6.9	192	1	CSR1_MOUSE	P97315 mus musculu	620	70.5	6.8	422	2	Q7Z4T1	Q7z4t1 homo sapien
548	71	6.9	195	2	Q9SL14	Q9sl14 arabisdopsis	621	70.5	6.8	428	2	Q8N9U5	Q8n9u5 homo sapien
549	71	6.9	201	2	Q70807	Q70807 tt virus. s	622	70.5	6.8	464	2	Q37899	Q37899 bacterioph
550	71	6.9	211	2	Q6QPM2	Q6qpm2 arabisdopsis	623	70.5	6.8	529	2	Q37899	Q37899 bacterioph
551	71	6.9	219	2	Q23219	Q23219 arabisdopsis	624	70.5	6.8	665	2	Q8BJH0	Q8bjh0 mus musculu
552	71	6.9	249	2	Q8CFL4	Q8cfl4 mus musculu	625	70.5	6.8	670	2	Q7MT53	Q7mt53 porphyromon
553	71	6.9	251	2	Q743S5	Q743s5 mycobacteri	626	70.5	6.8	677	2	Q7RVV0	Q7rvv0 neurospora
554	71	6.9	332	1	NPDI_MOUSE	Q64322 mus musculu	627	70.5	6.8	677	2	Q9HEH9	Q9heh9 neurospora
555	71	6.9	332	2	Q99JF9	Q99j69 mus musculu	628	70.5	6.8	720	2	Q9N003	Q9n003 macaca faec
556	71	6.9	370	2	Q8QK2	Q8qk2 fugu rubrip	629	70.5	6.8	731	2	Q6BWS4	Q6bws4 debaryomyce
557	71	6.9	372	2	Q7T0P0	Q7t0p0 xenopus lae	630	70.5	6.8	1034	2	Q6FWH6	Q6fwh6 candida gla
558	71	6.9	376	2	Q7MMW0	Q7mmw0 porphyromon	631	70.5	6.8	1064	2	Q6P7W6	Q6p7w6 mus musculu
559	71	6.9	391	2	Q8RQX6	Q8rxq6 cytophaga s	632	70.5	6.8	1125	2	Q6A098	Q6a098 mus musculu
560	71	6.9	398	1	CAR4_RHINI	Q03700 rhizopus ni	633	70.5	6.8	1129	2	Q6P4K6	Q6p4k6 xenopus tro
561	71	6.9	413	2	Q8YLT9	Q8ylt9 anabaena sp	634	70.5	6.8	1356	2	Q6A098	Q6a098 mus musculu
562	71	6.9	426	2	Q96JTV9	Q96jtv9 homo sapien	635	70.5	6.8	1449	2	Q8YF91	Q8yf91 mus musculu
563	71	6.9	441	2	Q6JK97	Q6jk97 neodiprion	636	70.5	6.8	1468	1	Q9V917	Q9v917 drosophila
564	71	6.9	445	1	ZG5_XENLA	P18725 xenopus lae	637	70.5	6.8	1733	2	Q9KI14	Q9ki14 staphylococ
565	71	6.9	445	2	Q95779	Q95779 homo sapien	638	70.5	6.8	1733	2	Q9KI14	Q9ki14 staphylococ
566	71	6.9	455	2	Q9D298	Q9d298 mus musculu	639	70	6.8	128	2	Q8V7C9	Q8v7c9 tt virus. o
567	71	6.9	455	2	Q9ESP5	Q9esp5 mus musculu	640	70	6.8	170	2	Q8BI21	Q8bi21 debaryomyce
568	71	6.9	459	2	Q8TBJ5	Q8tbj5 homo sapien	641	70	6.8	192	1	CSRI_RAT	CSRI_RAT
569	71	6.9	459	2	Q9BZ91	Q9bz91 homo sapien	642	70	6.8	192	2	Q9YGD7	Q9ygd7 rattus norv
570	71	6.9	462	2	Q91906	Q91906 xenopus lae	643	70	6.8	193	2	Q9D1M8	Q9d1m8 mus musculu
571	71	6.9	474	2	Q9AJH9	Q9ajh9 cytophaga s	644	70	6.8	257	2	Q7R1X9	Q7r1x9 giardia lam
572	71	6.9	497	2	Q8CG95	Q8cg95 mus musculu	645	70	6.8	260	2	Q7RJW0	Q7rjw0 plasmodium
573	71	6.9	498	2	Q95780	Q95780 homo sapien	646	70	6.8	294	2	Q9SVL2	Q9svl2 arabisdopsis
574	71	6.9	501	2	Q91BD0	Q91bd0 brachydanio	647	70	6.8	339	2	Q24699	Q24699 dugesia tig
575	71	6.9	510	2	Q8J2Z4	Q8j2z4 metallospha	648	70	6.8	339	2	Q80MW7	Q80mw7 mus musculu
576	71	6.9	524	1	GLPK_HUMAN	P32189 homo sapien	649	70	6.8	356	1	TRBM_BOVIN	TRBM_BOVIN
577	71	6.9	530	2	Q61Q27	Q61q27 homo sapien	650	70	6.8	372	2	Q96NB3	Q96nb3 homo sapien
578	71	6.9	534	2	Q7ZWE4	Q7zwe4 brachydanio	651	70	6.8	372	2	Q9CJ33	Q9cjb3 bovine vira
579	71	6.9	553	1	GP33_HUMAN	Q14409 homo sapien	652	70	6.8	385	2	Q8C2S3	Q8c2s3 mus musculu
580	71	6.9	553	2	Q6NXP9	Q6nxp9 homo sapien	653	70	6.8	389	2	Q58755	Q58755 pyrococcus
581	71	6.9	556	2	Q9HE97	Q9he97 neurospora	654	70	6.8	396	1	NHL1_RAT	NHL1_RAT
582	71	6.9	619	2	Q6CG09	Q6cg09 yarrowia li	655	70	6.8	397	2	Q6P4A9	Q6p4a9 homo sapien
583	71	6.9	722	1	GLNE_CRIGR	Q7tc49 c bifunctio	656	70	6.8	401	1	NHL1_MOUSE	NHL1_MOUSE
584	71	6.9	722	1	GLNE_MOUSE	Q91wg8 m bifunctio	657	70	6.8	402	1	KROS_AVISU	KROS_AVISU
585	71	6.9	722	1	GLNE_RAT	Q35826 r bifunctio	658	70	6.8	439	2	Q9DAMS	Q9dams avian sarco
586	71	6.9	787	2	Q8BI82	Q8bi82 mus musculu	659	70	6.8	449	2	Q6CEP6	Q6cep6 yarrowia li
587	71	6.9	788	2	Q9TUN3	Q9tun3 oryctolagus	660	70	6.8	458	2	Q9H731	Q9h731 homo sapien
588	71	6.9	827	2	Q8HFG9	Q8hfg9 mus musculu	661	70	6.8	460	2	Q8N7M1	Q8n7m1 drosophila
589	71	6.9	848	2	Q84HQ5	Q84hq5 helicobacte	662	70	6.8	468	1	WNTG_DROME	WNTG_DROME
590	71	6.9	857	2	Q62A28	Q62a28 cryptospori	663	70	6.8	484	2	Q9HCF7	Q9hcf7 homo sapien
591	71	6.9	955	2	Q62A28	Q62a28 burkholderi	664	70	6.8	520	2	Q75DG9	Q75dg9 ashbya gos
592	71	6.9	965	2	Q63NY9	Q63ny9 burkholderi	665	70	6.8	530	2	Q8P280	Q8p280 homo sapien
593	71	6.9	967	2	Q63HK3	Q63hk3 homo sapien	666	70	6.8	533	2	Q8PGV7	Q8pgv7 xanthomonas
594	71	6.9	974	2	Q68FE8	Q68fe8 mus musculu	667	70	6.8	566	2	Q7RYN8	Q7ryn8 neurospora
595	71	6.9	979	2	Q23096	Q23096 arabisdopsis	668	70	6.8	582	1	ZF36_HUMAN	ZF36_HUMAN
596	71	6.9	1067	2	Q9PFS1	Q9fsp1 arabisdopsis	669	70	6.8	619	2	Q960W5	Q960w5 drosophila
597	71	6.9	1171	2	Q80TF7	Q80tf7 mus musculu	670	70	6.8	737	2	Q8ND82	Q8nd82 homo sapien
598	71	6.9	1321	2	Q962D1	Q962d1 drosophila	671	70	6.8	784	2	Q97702	Q97702 canis fami
599	71	6.9	1323	2	Q7K3Z0	Q7ksz0 drosophila	672	70	6.8	784	2	Q9TUN7	Q9tun7 canis fami
600	71	6.9	1370	1	Z261_MOUSE	Q9jlm4 mus musculu	673	70	6.8	922	2	Q6BTJ4	Q6btj4 debaryomyce
601	71	6.9	1374	2	Q7YU77	Q7yu77 drosophila	674	70	6.8	947	1	MUSK_CHICK	MUSK_CHICK
602	71	6.9	1376	2	Q9VI63	Q9vi63 drosophila	675	70	6.8	976	1	RFOM_ARATH	RFOM_ARATH
603	71	6.9	1672	2	Q9SCJ9	Q9scj9 arabisdopsis	676	70	6.8	978	2	Q8BLJ5	Q8blj5 pseudomonas
604	71	6.9	3262	2	Q9EQ15	Q9eq15 mus musculu	677	70	6.8	1000	2	Q9KU57	Q9ku57 drosophila
605	71	6.9	23015	2	Q8IQ18	Q8iq18 drosophila	678	70	6.8	1009	2	Q9GZ11	Q9gz11 caenorhabdi
606	70.5	6.8	121	2	Q6SA01	Q6sa01 bombyx mori	679	70	6.8	1077	2	Q6AWM8	Q6awm8 drosophila
607	70.5	6.8	170	2	Q8BN10	Q8bn10 mus musculu	680	70	6.8	1240	2	Q7KU58	Q7ku58 drosophila
608	70.5	6.8	185	2	Q8VC80	Q8vc80 mus musculu	681	70	6.8	1594	1	SOL_DROME	SOL_DROME
609	70.5	6.8	186	2	Q8QQV6	Q8qqv6 minute viru	682	70	6.8	1683	2	Q7Z5J5	Q7z5j5 mus sapien
610	70.5	6.8	213	2	Q693P5	Q693p5 helicoverpa	683	70	6.8	1884	2	Q7S737	Q7s737 neurospora
611	70.5	6.8	234	2	Q7WTT9	Q7wt9 shewanella	684	70	6.8	2476	1	ATRX_MOUSE	ATRX_MOUSE
612	70.5	6.8	267	2	P90673	P90673 artemia san	685	70	6.8	2809	2	Q7R041	Q7r041 giardia lam
613	70.5	6.8	274	2	Q88PH4	Q88ph4 pseudomonas	686	69.5	6.7	155	2	Q8T926	Q8t926 tetrabymena
614	70.5	6.8	329	1	IPNS_STRJU	P18286 streptomyce	687	69.5	6.7	183	2	Q8S3W8	Q8s3w8 hordeum vul
615	70.5	6.8	350	2	Q9LY80	Q9ly80 arabisdopsis	688	69.5	6.7	193	2	Q6DEQ0	Q6deq0 xenopus tro

689 69.5 6.7 264 2 Q6A6V9 Q6a6v9 propionibac
 690 69.5 6.7 282 2 Q91TR4 Q91tr4 tupaidid her
 691 69.5 6.7 310 1 SDCL HUMAN P18827 homo sapien
 692 69.5 6.7 315 2 Q6VQT1 Q6vqt1 pseudomonas
 693 69.5 6.7 326 2 Q74DF2 Q74df2 glycobacter s
 694 69.5 6.7 356 2 Q6Z4U1 Q6z4u1 oryza sativ
 695 69.5 6.7 356 2 Q7DFZ5 Q7dfz5 edwardsiell
 696 69.5 6.7 359 1 SIA9_MOUSE O88829 mus musculus
 697 69.5 6.7 374 1 PST1_MYCTU P15712 mycobacteri
 698 69.5 6.7 374 2 Q7U0Z8 Q7u0z8 mycobacteri
 699 69.5 6.7 386 2 Q8KHC4 Q8khc4 pseudomonas
 700 69.5 6.7 387 2 Q9CZ65 Q9cz65 mus musculus
 701 69.5 6.7 422 2 Q8BZ34 Q8bz34 mus musculus
 702 69.5 6.7 440 2 Q7PWF9 Q7pwf9 anopheles g
 703 69.5 6.7 443 2 Q8LFFN4 Q8lfn4 arabidopsis
 704 69.5 6.7 449 2 Q949U2 Q949u2 arabidopsis
 705 69.5 6.7 474 2 Q7PWD1 Q7pwd1 anopheles g
 706 69.5 6.7 554 2 Q9LSH8 Q9lsh8 arabidopsis
 707 69.5 6.7 613 2 Q8EN76 Q8en76 oceanobacil
 708 69.5 6.7 623 2 Q8XVB0 Q8xvb0 ralstonia s
 709 69.5 6.7 627 1 2442 HUMAN Q9h7r0 homo sapien
 710 69.5 6.7 646 2 Q9GNA1 Q9gnal leishmania
 711 69.5 6.7 648 2 Q6DI55 Q6di55 mus musculus
 712 69.5 6.7 675 2 Q8I179 Q8i179 drosophila
 713 69.5 6.7 714 2 Q8PG61 Q8pg61 xanthomonas
 714 69.5 6.7 922 2 Q8BSH0 Q8bsh0 mus musculus
 715 69.5 6.7 1042 2 P90974 P90974 caenorhabdi
 716 69.5 6.7 1059 1 AN28 HUMAN O15084 homo sapien
 717 69.5 6.7 1063 2 Q65442 Q65442 pestivirus
 718 69.5 6.7 1087 1 E4L3 HUMAN Q9Y2J2 homo sapien
 719 69.5 6.7 1103 2 Q9456 Q9456 arabidopsis
 720 69.5 6.7 1246 2 Q9NEE0 Q9nee0 leishmania
 721 69.5 6.7 1326 2 Q8A3Q7 Q8a3q7 bacteroides
 722 69.5 6.7 1366 2 Q69Z41 Q69z41 mus musculus
 723 69.5 6.7 1670 1 CA34 HUMAN Q01955 homo sapien
 724 69.5 6.7 1693 1 RGNE_MOUSE P97433 mus musculus
 725 69.5 6.7 3973 2 Q65786 Q65786 bovine vira
 726 69.5 6.7 4226 2 Q8TKD6 Q8tkd6 methanosarc
 727 69 6.7 123 2 Q80PV5 Q80pv5 porcine rep
 728 69 6.7 147 2 Q9BLW5 Q9blw5 heliothis v
 729 69 6.7 148 2 Q8VQH6 Q8vqh6 uncultured
 730 69 6.7 149 2 Q8VQH5 Q8vqh5 uncultured
 731 69 6.7 151 1 HSPH_BRAJA O66110 bradyrhizob
 732 69 6.7 160 2 Q8N912 Q8n912 homo sapien
 733 69 6.7 166 2 Q66TY7 Q66ty7 culicoides
 734 69 6.7 178 2 Q8KBV4 Q8kbv4 chlorobium
 735 69 6.7 181 2 Q8GP96 Q8gp96 caenorhabdi
 736 69 6.7 181 2 Q9V5Z3 Q9v5z3 drosophila
 737 69 6.7 188 2 Q95T42 Q95t42 drosophila
 738 69 6.7 192 1 CSR2_HUMAN Q15527 homo sapien
 739 69 6.7 192 1 CSR2_MOUSE P97314 mus musculus
 740 69 6.7 192 1 CSR2_RAT Q62908 rattus norv
 741 69 6.7 193 2 Q71V27 Q71v27 mus musculus
 742 69 6.7 239 2 Q8TCD0 Q8tcd0 homo sapien
 743 69 6.7 258 1 C4BB_RAT Q63515 rattus norv
 744 69 6.7 265 2 Q8LV07 Q8lv07 arabidopsis
 745 69 6.7 308 1 SIN2_ARATH Q9mzp4 arabidopsis
 746 69 6.7 330 2 Q9H861 Q9h861 homo sapien
 747 69 6.7 333 2 Q8GXL3 Q8gx13 arabidopsis
 748 69 6.7 348 1 Z134_HUMAN P52741 homo sapien
 749 69 6.7 352 2 Q72Zr6 Q72zr6 bacillus ce
 750 69 6.7 372 2 Q9YK08 Q9yk08 bovine vira
 751 69 6.7 373 2 Q8A7A9 Q8a7a9 bacteroides
 752 69 6.7 380 2 Q6T5A6 Q6t5a6 campylobact
 753 69 6.7 383 2 Q888J0 Q888j0 pseudomonas
 754 69 6.7 408 2 Q94I85 Q94i85 oryza sativ
 755 69 6.7 418 2 Q8PEI7 Q8pei7 xanthomonas
 756 69 6.7 423 2 Q8NG30 Q8ng30 corynebacte
 757 69 6.7 427 2 Q9Y4B2 Q9y4b2 homo sapien
 758 69 6.7 427 2 Q7UUh3 Q7uuh3 rhodopirell
 759 69 6.7 462 2 Q8NHZ0 Q8nhz0 homo sapien
 760 69 6.7 462 2 Q9H9P0 Q9h9p0 homo sapien
 761 69 6.7 489 2 Q6PJ68 Q6pj68 homo sapien

762 69 6.7 494 2 Q6PUJ4 Q6puj4 homo sapien
 763 69 6.7 524 2 Q8AVN9 Q8avn9 xenopus lae
 764 69 6.7 534 2 Q6ZMX8 Q6zmx8 homo sapien
 765 69 6.7 540 2 Q9VU53 Q9vu53 drosophila
 766 69 6.7 544 2 Q6AW86 Q6aw86 homo sapien
 767 69 6.7 544 2 Q6ZS42 Q6zs42 homo sapien
 768 69 6.7 550 2 Q7Q2D0 Q7q2d0 anopheles g
 769 69 6.7 553 1 Z324_HUMAN O75467 homo sapien
 770 69 6.7 581 2 Q922Q3 Q922q3 mus musculus
 771 69 6.7 608 2 Q8TF54 Q8tf54 homo sapien
 772 69 6.7 615 2 Q8YFA5 Q8yfa5 anabaena sp
 773 69 6.7 629 2 Q9UIQ3 Q9ulq3 caenorhabdi
 774 69 6.7 658 2 Q8OV96 Q8ov96 mus musculus
 775 69 6.7 659 1 Z304_HUMAN Q9hcx3 homo sapien
 776 69 6.7 672 2 Q9WVH4 Q9wvh4 mus musculus
 777 69 6.7 675 1 ZG20_XENLA P18714 xenopus lae
 778 69 6.7 682 1 ZN45_HUMAN Q02386 homo sapien
 779 69 6.7 683 2 Q6CLD9 Q6cld9 kluyveromyc
 780 69 6.7 689 1 Q7QFT5 Q7qft5 anopheles g
 781 69 6.7 788 1 ITB3_HUMAN P05106 homo sapien
 782 69 6.7 927 2 Q823X9 Q823x9 chlamydophi
 783 69 6.7 939 2 Q8WFX1 Q8wfx1 paracentrot
 784 69 6.7 1013 2 Q9W263 Q9w263 drosophila
 785 69 6.7 1026 1 PTP1_CAEEL P28191 caenorhabdi
 786 69 6.7 1092 2 Q8IVE8 Q8ive8 homo sapien
 787 69 6.7 1299 2 Q9STE0 Q9ste0 brassica na
 788 69 6.7 1351 2 Q7TQ28 Q7tq28 mus musculus
 789 69 6.7 1352 2 Q82KP3 Q82kp3 streptomyce
 790 69 6.7 1374 2 Q9VSU0 Q9vsu0 drosophila
 791 69 6.7 1449 2 Q9UI12 Q9ui12 drosophila
 792 69 6.7 1450 2 Q8IOB8 Q8iob8 drosophila
 793 69 6.7 1462 2 Q9UI13 Q9ui13 drosophila
 794 69 6.7 1616 2 Q7TQ29 Q7tq29 mus musculus
 795 69 6.7 1646 2 Q7TQ27 Q7tq27 mus musculus
 796 69 6.7 1659 2 Q8IWQ9 Q8iww9 homo sapien
 797 69 6.7 1674 2 Q7TPQ3 Q7tpq3 mus musculus
 798 69 6.7 2228 2 Q9VN58 Q9vn58 drosophila
 799 69 6.7 2382 2 Q9BI19 Q9bi19 drosophila
 800 69 6.7 2387 2 Q6HZ36 Q6hz36 bos taurus
 801 69 6.7 2409 2 Q96OG6 Q96og6 drosophila
 802 69 6.7 2786 2 Q9VSU2 Q9vsu2 drosophila
 803 69 6.7 3448 2 Q6TVI3 Q6tlv3 bovine vira
 804 69 6.7 116 2 Q6C917 Q6c917 yarrowia li
 805 69 6.7 135 1 VE6_PAPVE P11331 european el
 806 69 6.7 150 2 Q9WQH1 Q9wqh1 tt virus. h
 807 69 6.7 157 2 Q8NMZ0 Q8nmz0 corynebacte
 808 69 6.7 161 2 Q6ZQN1 Q6zqn1 homo sapien
 809 69 6.7 174 2 Q9L369 Q9l369 acinetobact
 810 69 6.7 191 1 CSR1_CHICK P67966 gallus gall
 811 69 6.7 191 1 CSR1_CONJA P67967 coturnix co
 812 69 6.7 191 2 Q86DH9 Q86dh9 aplysia cal
 813 69 6.7 200 2 Q82DX3 Q82dx3 streptomyce
 814 69 6.7 211 2 Q9XAR2 Q9xar2 streptomyce
 815 69 6.7 228 2 Q8IF50 Q8if50 trypanosoma
 816 69 6.7 273 2 Q9RUE5 Q9ru5 deinococcus
 817 69 6.7 277 1 ANGL_EMENI Q00746 emericella
 818 69 6.7 288 2 Q85489 Q85489 rhodococcus
 819 69 6.7 295 1 WR46_ARATH Q9skd9 arabidopsis
 820 69 6.7 351 2 Q6YIS2 Q6yis2 fer-de-lanc
 821 69 6.7 352 2 Q8MR10 Q8mr10 drosophila
 822 69 6.7 365 2 Q7T3A5 Q7t3a5 brachydanio
 823 69 6.7 372 2 Q6MZG1 Q6mzg1 homo sapien
 824 69 6.7 373 2 Q92BH0 Q92bh0 listeria in
 825 69 6.7 386 2 Q7ZOG7 Q7z0g7 halocynthia
 826 69 6.7 390 2 Q98BD3 Q98bd3 thizobium l
 827 69 6.7 391 2 Q8RQW4 Q8rqw4 cytophaga s
 828 69 6.7 391 2 Q8RR08 Q8rr08 cytophaga s
 829 69 6.7 391 2 Q8RR09 Q8rr09 cytophaga s
 830 69 6.7 391 2 Q8RR10 Q8rr10 cytophaga s
 831 69 6.7 391 2 Q8RR11 Q8rr11 cytophaga s
 832 69 6.7 391 2 Q8RR12 Q8rr12 cytophaga s
 833 69 6.7 391 2 Q8RR13 Q8rr13 cytophaga s
 834 69 6.7 391 2 Q8RR14 Q8rr14 cytophaga s

835	68.5	6.6	391	2	Q8RR15	Q8rr15 cytophaga s	908	68	6.6	363	2	Q8RLN0	Q8rln0 mus musculo
836	68.5	6.6	391	2	Q8RR16	Q8rr16 cytophaga s	909	68	6.6	363	2	Q8CWV9	Q8cwy9 mus musculo
837	68.5	6.6	409	2	Q6AH36	Q6ah36 leifsonia x	910	68	6.6	363	2	Q9CYI6	Q9cyl6 mus musculo
838	68.5	6.6	436	2	Q7QR05	Q7qr05 giardia lam	911	68	6.6	383	2	Q8SWI8	Q8swi8 encephalito
839	68.5	6.6	447	2	Q7RRF3	Q7rrf3 plasmodium	912	68	6.6	383	2	Q6FCQ4	Q6fcq4 acinetobact
840	68.5	6.6	466	2	Q7QACA6	Q7qac6 geobacter s	913	68	6.6	385	2	Q9SXF5	Q9sxf5 lithospermu
841	68.5	6.6	468	1	F1Z1 BOVIN	P50448 bos taurus	914	68	6.6	403	2	Q6ZQU7	Q6zqu7 homo sapien
842	68.5	6.6	476	2	Q1LCK4	Q1lck4 rikenella m	915	68	6.6	424	2	Q7SXY9	Q7sxy9 brachydanio
843	68.5	6.6	483	2	Q95FP3	Q95fp3 mollugo ver	916	68	6.6	467	2	Q941V5	Q941v5 oryza sativ
844	68.5	6.6	515	2	Q8JH80	Q8jh80 xenopus lae	917	68	6.6	474	2	Q88SV1	Q88sv1 lactobacill
845	68.5	6.6	528	2	P87239	P87239 schizosacch	918	68	6.6	493	2	Q9BN02	Q9bn02 drosophila
846	68.5	6.6	568	2	Q71TB1	Q71tb1 bacterioph	919	68	6.6	499	1	YL11 MYCHO	P43055 mycoplasma
847	68.5	6.6	582	2	Q7Q5B0	Q7q5b0 anopheles g	920	68	6.6	504	1	Z273_HUMAN	Q14593 homo sapien
848	68.5	6.6	590	2	Q7QMN3	Q7qmn3 anopheles g	921	68	6.6	510	1	YD1D_SCHPO	O13692 schizosacch
849	68.5	6.6	596	2	Q80XN4	Q80xn4 mus musculo	922	68	6.6	513	2	O52602	O52602 sulfolobus
850	68.5	6.6	617	2	Q8OT67	Q8ot67 mus musculo	923	68	6.6	513	2	Q974R7	Q974r7 sulfolobus
851	68.5	6.6	634	2	Q6NND3	Q6nnd3 drosophila	924	68	6.6	522	2	Q7XJN9	Q7xjn9 arabidopsis
852	68.5	6.6	634	2	Q9VH18	Q9vhl8 drosophila	925	68	6.6	524	1	GLPK RAT	O63060 rattus norv
853	68.5	6.6	653	1	Z274_HUMAN	Q9vhl8 drosophila	926	68	6.6	524	2	O42147	O42147 xenopus lae
854	68.5	6.6	657	2	Q7MRE4	Q7mre4 wolfinella s	927	68	6.6	537	2	Q94FM5	Q94fm5 nicotiana t
855	68.5	6.6	666	2	Q7Z3W5	Q7z3w5 homo sapien	928	68	6.6	541	2	Q725M3	Q725m3 desulfovibr
856	68.5	6.6	671	2	Q6BJY7	Q6bjy7 debaryomyce	929	68	6.6	541	2	Q7S2B4	Q7sze4 brachydanio
857	68.5	6.6	687	2	Q8X088	Q8x088 neurospora	930	68	6.6	563	2	Q7SZX6	Q7szx6 brachydanio
858	68.5	6.6	687	2	Q6ZT57	Q6zt57 homo sapien	931	68	6.6	587	2	Q8N3N5	Q8n3n5 homo sapien
859	68.5	6.6	720	2	O69273	O69273 corynebacte	932	68	6.6	591	1	PAX1_HUMAN	P49023 homo sapien
860	68.5	6.6	730	2	Q7PW73	Q7pw73 anopheles g	933	68	6.6	600	2	Q96HY1	Q96hy1 homo sapien
861	68.5	6.6	788	2	Q6BVD1	Q6bvd1 debaryomyce	934	68	6.6	600	2	Q9H0F9	Q9h0f9 homo sapien
862	68.5	6.6	794	2	Q7XKV1	Q7xkv1 oryza sativ	935	68	6.6	600	2	Q9CWS4	Q9cws4 m mus muscu
863	68.5	6.6	812	2	Q8N272	Q8n272 streptomyce	936	68	6.6	619	2	Q9NYK3	Q9nyk3 homo sapien
864	68.5	6.6	821	2	Q96JF6	Q96jff6 homo sapien	937	68	6.6	624	2	Q9U3N7	Q9u3n7 caenorhabdi
865	68.5	6.6	824	2	Q8P4W1	Q8p4w1 xanthomonas	938	68	6.6	625	2	Q6CNE7	Q6cne7 kluyveromye
866	68.5	6.6	829	2	Q9WRT9	Q9wrt9 macaca mula	939	68	6.6	647	1	SSY1 WHEAT	Q63654 triticum ae
867	68.5	6.6	893	1	DR14 ARATH	Q9si85 arabidopsis	940	68	6.6	647	2	Q9LEGO	Q9lec0 triticum ae
868	68.5	6.6	908	2	Q7S6B3	Q7s6b3 neurospora	941	68	6.6	647	2	Q9SQG9	Q9sqg9 triticum ae
869	68.5	6.6	953	2	Q8MQR4	Q8mqr4 drosophila	942	68	6.6	647	2	Q9SOHQ	Q9sqh0 agelophor
870	68.5	6.6	954	2	Q67T41	Q67t41 symbiobacte	943	68	6.6	664	2	Q90YK2	Q90yk2 xiphophorus
871	68.5	6.6	974	2	P91658	P91658 drosophila	944	68	6.6	665	2	Q8BI96	Q8bi96 mus musculo
872	68.5	6.6	983	2	Q75039	Q75039 homo sapien	945	68	6.6	665	2	Q811F1	Q811f1 mus musculo
873	68.5	6.6	1005	2	Q750J0	Q750j0 ashbya goss	946	68	6.6	691	2	O43361	O43361 homo sapien
874	68.5	6.6	1024	1	TIPT DROME	Q9u3v5 drosophila	947	68	6.6	719	2	Q7JMK7	Q7jmk7 caenorhabdi
875	68.5	6.6	1309	2	Q9VIV0	Q9vivo drosophila	948	68	6.6	721	1	GA56_HUMAN	Q14393 homo sapien
876	68.5	6.6	1421	2	Q9SXQ5	Q9sxq5 arabidopsis	949	68	6.6	722	1	GLNE_HUMAN	Q9Y223 h bifunctio
877	68.5	6.6	1638	2	Q8IWQ7	Q8iwq7 homo sapien	950	68	6.6	722	2	Q6QNY6	Q6qny6 homo sapien
878	68.5	6.6	1638	2	Q86XX2	Q86xx2 homo sapien	951	68	6.6	722	2	Q6QNY7	Q6qny7 homo sapien
879	68.5	6.6	1596	1	PKX5 BRACL	Q9n1l5 branchiost	952	68	6.6	729	2	Q7QES2	Q7qes2 anopheles g
880	68.5	6.6	1701	2	Q7SCH8	Q7sch8 neurospora	953	68	6.6	729	2	Q8AVI6	Q8avi6 xenopus lae
881	68.5	6.6	1719	2	Q86XX3	Q86xx3 homo sapien	954	68	6.6	796	1	YRS7 CAEEL	O10003 caenorhabdi
882	68.5	6.6	2085	2	Q7R322	Q7r322 giardia lam	955	68	6.6	802	2	Q6DF97	Q6df97 xenopus lae
883	68.5	6.6	2254	2	Q6ZM94	Q6zm94 brachydanio	956	68	6.6	865	2	Q7XEP9	Q7xep9 oryza sativ
884	68.5	6.6	2871	1	PBN1 BOVIN	P98133 bos taurus	957	68	6.6	886	2	Q653V4	Q653v4 oryza sativ
885	68.5	6.6	3587	2	Q6RKK6	Q6rkk6 gibberella	958	68	6.6	897	2	Q7XX33	Q7xx33 oryza sativ
886	68	6.6	95	2	Q6GPF94	Q6gpf94 caenorhabdi	959	68	6.6	903	2	Q8TLV6	Q8tly6 methanosarc
887	68	6.6	113	2	Q9GPP95	Q9gpp95 caenorhabdi	960	68	6.6	910	2	Q94MV0	Q94my0 haemophilus
888	68	6.6	123	2	Q855W9	Q855w9 mycobacteri	961	68	6.6	930	2	Q7T5D7	Q7t5d7 cercopithe
889	68	6.6	142	2	Q8ABJ5	Q8abj5 bacteroides	962	68	6.6	997	2	Q7T5D7	Q7t5d7 cercopithe
890	68	6.6	155	2	Q6A118	Q6a118 homo sapien	963	68	6.6	1005	2	Q805Z0	Q805z0 cercopithe
891	68	6.6	174	2	Q7VOT2	Q7vot2 prochloroco	964	68	6.6	1054	2	Q6GPM1	Q6gpm1 xenopus lae
892	68	6.6	191	2	Q6ZMS3	Q6zms3 homo sapien	965	68	6.6	1073	2	Q6AHV0	Q6ahv0 pneumocysti
893	68	6.6	194	1	CSR3_HUMAN	P50461 homo sapien	966	68	6.6	1090	1	GUXB_CELFI	P50899 cellulomona
894	68	6.6	194	1	CSR3_MOUSE	P50462 mus musculo	967	68	6.6	1137	2	Q6IRN0	Q6irn0 xenopus lae
895	68	6.6	197	2	Q64D93	Q64d93 uncultured	968	68	6.6	1137	2	Q01816	Q01816 pneumocysti
896	68	6.6	244	1	CUTC_PASMU	Q9cna6 pasteurella	969	68	6.6	1251	2	O45671	O45671 caenorhabdi
897	68	6.6	258	2	Q701H4	Q701h4 chimpanzee	970	68	6.6	1287	2	Q7Y212	Q7y212 cryptospori
898	68	6.6	281	2	Q91LB4	Q91lb4 white spot	971	68	6.6	1299	2	Q36489	Q36489 spodoptera
899	68	6.6	284	2	Q95878	Q95878 homo sapien	972	68	6.6	1383	2	Q86YV5	Q86yv5 homo sapien
900	68	6.6	291	1	NANK_ECOLI	P45425 escherichia	973	68	6.6	1724	2	Q7XSO7	Q7xso7 oryza sativ
901	68	6.6	301	2	Q8T3H7	Q8t3h7 drosophila	974	68	6.6	1889	1	RA11_MOUSE	Q61818 mus musculo
902	68	6.6	301	2	Q8BYV8	Q8byv8 mus musculo	975	68	6.6	2344	2	Q86117	Q86117 rabbit hemo
903	68	6.6	312	2	Q9NWE8	Q9nwe8 homo sapien	976	68	6.6	2479	2	Q63002	Q63002 rattus norv
904	68	6.6	317	2	Q74NR0	Q74nr0 bacillus ce	977	68	6.6	2543	2	Q81BR8	Q81br8 plasmodium
905	68	6.6	319	2	Q9VDQ5	Q9vdq5 drosophila	978	68	6.6	7667	2	Q7QG88	Q7qg88 anopheles g
906	68	6.6	341	2	O34434	O34434 bacillus su	979	67.5	6.5	123	3	Q805R5	Q805r5 porcine rep
907	68	6.6	355	2	Q8UCL6	Q8ucl6 agrobacteri	980	67.5	6.5	123	2	Q80Pv1	Q80pvl porcine rep

981	67.5	137	2	Q855S2	Q855s2 mycobacteri	1054	67.5	6.5	2647	1	FLNA HUMAN	P21333 homo sapien
982	67.5	144	2	Q81KA6	Q81ka6 drosophila	1055	67.5	6.5	2651	2	Q8NF52	Q8nf52 homo sapien
983	67.5	185	1	BX5S_MOUSE	Q88c75 mus musculus	1056	67.5	6.5	3014	2	Q39928	Q39928 hepatitis c
984	67.5	185	1	Q8C9H4	Q8c9h4 mus musculus	1057	67	6.5	128	2	Q8V7C7	Q8v7c7 tt virus. o
985	67.5	193	1	C8R2_CHICK	P50460 gallus gall	1058	67	6.5	131	2	Q61K23	Q61k23 drosophila
986	67.5	193	1	C8R2_COTUA	Q51588 turnix co	1059	67	6.5	133	2	Q60909	Q60909 mus musculus
987	67.5	193	1	Q842P4	Q642p4 xenopus lae	1060	67	6.5	140	2	Q99A26	Q99a26 bovine vira
988	67.5	263	2	Q8LV60	Q91v60 arabidopsis	1061	67	6.5	142	2	Q8WPI2	Q8wp12 boophilus m
989	67.5	267	2	Q8ZQR1	Q6zqr1 homo sapien	1062	67	6.5	150	2	Q96911	Q96911 human herpe
990	67.5	291	2	Q8ZB64	Q8ze64 streptomyce	1063	67	6.5	151	2	Q7PJ69	Q7pj69 anopheles g
991	67.5	310	2	Q7QK35	Q7qk35 anopheles g	1064	67	6.5	166	2	Q66TY9	Q66ty9 culicoides
992	67.5	321	2	Q8SXF3	Q8sxf3 drosophila	1065	67	6.5	181	2	Q7X723	Q7x723 oryza sativ
993	67.5	323	2	Q8N306	Q8n306 homo sapien	1066	67	6.5	185	2	Q8P384	Q8p384 xanthomonas
994	67.5	323	2	Q8TAG8	Q8tag8 homo sapien	1067	67	6.5	194	2	Q6DUZ5	Q6duz5 gekko japon
995	67.5	348	2	Q84U04	Q64u04 bacteroides	1068	67	6.5	223	2	Q8BLT1	Q8blt1 mus musculus
996	67.5	349	2	Q8AYD6	Q6ayd6 rattus norv	1069	67	6.5	229	2	Q6UNH7	Q6unh7 opuntia vir
997	67.5	358	2	Q6TWR3	Q6twp3 lemur catta	1070	67	6.5	236	2	Q8BJN9	Q8bjn9 mus musculus
998	67.5	360	2	Q6TYP8	Q6typ8 hafnia alve	1071	67	6.5	264	2	Q83834	Q83834 treponema p
999	67.5	378	2	Q8DM68	Q8dm68 synechococc	1072	67	6.5	283	2	Q8BIB1	Q8bib1 mus musculus
1000	67.5	380	2	Q8W403	Q8w403 drosophila	1073	67	6.5	297	2	Q31822	Q31822 bacillus su
1001	67.5	381	2	Q8JIT5	Q8jit5 xenopus lae	1074	67	6.5	321	2	Q7ZVD4	Q7zyd4 xenopus lae
1002	67.5	395	1	CARP_SYNRA	P81214 synccephalas	1075	67	6.5	340	1	TORS_DROME	Q77277 drosophila
1003	67.5	405	2	Q6NUJ6	Q6nuj6 homo sapien	1076	67	6.5	340	2	Q8WPE1	Q8wpel aplysia kur
1004	67.5	412	2	Q45301	Q45301 caenorhabdi	1077	67	6.5	366	1	YRO7_CABEL	Q9424 caenorhabdi
1005	67.5	414	1	SPYA_FELCA	P41689 felis silve	1078	67	6.5	378	2	Q99LE7	Q99le7 mus musculus
1006	67.5	419	2	Q82449	Q82449 arabidopsis	1079	67	6.5	392	2	Q9H807	Q9h807 homo sapien
1007	67.5	439	2	Q8N9G0	Q8n9g0 homo sapien	1080	67	6.5	394	2	Q8DAY9	Q8day9 vibrio vuln
1008	67.5	445	1	HPDP_ARATH	P93836 arabidopsis	1081	67	6.5	405	2	Q6B093	Q6b093 homo sapien
1009	67.5	454	2	Q6GUM2	Q6gum2 botrytis ci	1082	67	6.5	408	2	Q8BV67	Q8bv67 mus musculus
1010	67.5	464	2	Q6QGE2	Q6qge2 bacterioph	1083	67	6.5	421	2	Q9NXS0	Q9nxso homo sapien
1011	67.5	470	2	Q845X4	Q845x4 cellulophag	1084	67	6.5	421	2	Q95RS6	Q95rs6 drosophila
1012	67.5	474	2	Q8EZA9	Q8eza9 bacillus co	1085	67	6.5	422	2	Q18317	Q18317 caenorhabdi
1013	67.5	498	2	Q8BW35	Q8bw35 mus musculus	1086	67	6.5	430	2	Q9DGC4	Q9dgc4 brachydanio
1014	67.5	561	2	Q8VJ24	Q8vj24 drosophila	1087	67	6.5	438	2	Q90ZT2	Q90z2 brachydanio
1015	67.5	564	2	Q8BJ29	Q8bj29 mus musculus	1088	67	6.5	438	2	Q804Q5	Q804q5 brachydanio
1016	67.5	594	2	P31805	Q91805 sarcophaga	1089	67	6.5	452	2	Q9LT78	Q9lt78 arabidopsis
1017	67.5	595	1	ZN85_HUMAN	P03923 homo sapien	1090	67	6.5	479	2	Q96JV1	Q96jv1 homo sapien
1018	67.5	598	2	Q89YG9	Q89yg9 homo sapien	1091	67	6.5	480	2	Q7UWN4	Q7uwn4 rhodopirell
1019	67.5	602	2	Q9VFD9	Q9vfd9 drosophila	1092	67	6.5	495	1	PUR1_SYN3	Q55621 synechocyst
1020	67.5	619	2	Q6CAJ0	Q6caj0 yarrowia li	1093	67	6.5	498	2	Q8TC21	Q8tc21 homo sapien
1021	67.5	625	2	Q19240	Q19240 caenorhabdi	1094	67	6.5	510	2	Q8TEI2	Q8te12 homo sapien
1022	67.5	633	2	Q7RAG2	Q7rag2 plasmodium	1095	67	6.5	516	1	ZG53_XENLA	P18728 xenopus lae
1023	67.5	639	2	Q77133	Q77133 caenorhabdi	1096	67	6.5	517	2	Q9P2I8	Q9p2i8 homo sapien
1024	67.5	639	2	Q95QMS	Q95qms caenorhabdi	1097	67	6.5	534	2	Q94FM4	Q94fm4 nicotiana t
1025	67.5	647	2	Q8C168	Q8ci68 mus musculus	1098	67	6.5	538	2	Q6ZS47	Q6zsa7 homo sapien
1026	67.5	650	2	Q8C168	Q8c168 mus musculus	1099	67	6.5	543	2	Q8IGL8	Q8igl8 drosophila
1027	67.5	661	2	Q8BYC3	Q8byc3 mus musculus	1100	67	6.5	557	2	Q8VI37	Q8vi37 mus musculus
1028	67.5	668	2	Q7QHZ8	Q7qhz8 anopheles g	1101	67	6.5	583	1	AXU1_MOUSE	P59054 mus musculus
1029	67.5	697	2	Q8PDU2	Q8pdu2 xanthomonas	1102	67	6.5	586	2	Q66H76	Q66h76 rattus norv
1030	67.5	705	2	Q8N823	Q8n823 homo sapien	1103	67	6.5	591	2	Q8VI36	Q8vi36 mus musculus
1031	67.5	739	1	DCLY_HAFAL	P05033 hafnia alve	1104	67	6.5	613	2	Q7T246	Q7t246 xenopus lae
1032	67.5	743	1	Z267_HUMAN	Q14586 homo sapien	1105	67	6.5	616	2	Q6PUW8	Q6pjw8 homo sapien
1033	67.5	761	2	Q38708	Q38708 alnus glut	1106	67	6.5	625	2	Q8KC38	Q8kc38 chlorobium
1034	67.5	838	2	Q36C61	Q96c61 homo sapien	1107	67	6.5	648	2	Q87114	Q87114 neurospora
1035	67.5	858	2	Q81XK0	Q8ixk0 homo sapien	1108	67	6.5	652	2	Q74JD8	Q74jd8 lactobacill
1036	67.5	882	2	Q8UGQ1	Q8ugq1 agrobacteri	1109	67	6.5	706	1	ECL6_HUMAN	P41182 homo sapien
1037	67.5	983	2	Q6NXXF1	Q6nxf2 homo sapien	1110	67	6.5	706	1	Z225_HUMAN	Q9uk10 homo sapien
1038	67.5	1007	2	Q8EHB9	Q8eb9 shewanella	1111	67	6.5	707	2	ECL6_MOUSE	P41183 mus musculus
1039	67.5	1047	2	Q6G4M6	Q6g4m6 bartonella	1112	67	6.5	707	2	Q8CB25	Q8cb25 mus musculus
1040	67.5	1083	2	Q8QFO7	Q8qf7 gallus gall	1113	67	6.5	722	2	Q6QMY5	Q6qmy5 homo sapien
1041	67.5	1122	2	Q8SXD4	Q8sxd4 drosophila	1114	67	6.5	725	2	Q96MR5	Q96mr5 mus sapien
1042	67.5	1149	2	Q6C0A2	Q6c0a2 yarrowia li	1115	67	6.5	725	2	Q8EWM4	Q8ewa4 mycoplasma
1043	67.5	1161	2	Q6BJZ1	Q6bjz1 mus musculus	1116	67	6.5	738	2	Q9ULA1	Q9ula1 homo sapien
1044	67.5	1240	2	Q6BUST3	Q6bet3 debaryomyce	1117	67	6.5	742	2	Q8IBV3	Q8ibv3 giardia lam
1045	67.5	1268	2	Q8ULI3	Q9uli3 homo sapien	1118	67	6.5	757	1	KNC3_HUMAN	Q14003 homo sapien
1046	67.5	1455	2	Q8TES4	Q8tes4 homo sapien	1119	67	6.5	799	1	KNC3_MOUSE	Q61409 mus musculus
1047	67.5	1461	2	Q95Z59	Q95z59 plasmodium	1120	67	6.5	825	2	Q28477	Q28477 macaca fasc
1048	67.5	1461	2	Q7KQK4	Q7kqk4 plasmodium	1121	67	6.5	855	2	Q82HF9	Q82hf9 streptomyce
1049	67.5	1544	2	Q8MQW0	Q8mqw0 drosophila	1122	67	6.5	956	1	SVI_AQUAE	Q66651 aquifex aeo
1050	67.5	1641	2	Q41700	Q41700 vicia sativ	1123	67	6.5	969	2	Q7RTU1	Q7ryul neurospora
1051	67.5	2077	1	TEGU_HHV6G	P30002 human herpe	1124	67	6.5	979	2	Q6N043	Q6n043 homo sapien
1052	67.5	2119	2	Q6CDZ4	Q6cdz4 yarrowia li	1125	67	6.5	995	2	Q9HC18	Q9hc18 homo sapien
1053	67.5	2161	2	Q9E1F1	Q9e1f1 meleagrid h	1126	67	6.5	1012	1	DPOL_HHV7J	P52342 human herpe

1127	67	6.5	1013	2	O92827	O92827 human herpe	1200	66.5	6.4	803	1	ZB17_HUMAN	Q13105 homo sapien
1128	67	6.5	1014	2	Q8BL89	Q8BL89 mus musculu	1201	66.5	6.4	841	2	Q8H4E4	Q8H4P4 oryza sativ
1129	67	6.5	1017	1	L6G1_YEAST	P35688 saccharomyc	1202	66.5	6.4	896	2	Q9VUR6	Q9VUR6 drosophila
1130	67	6.5	1025	2	Q6WZM6	Q6WZM6 homo sapien	1203	66.5	6.4	907	1	SYA_BDEBA	P61698 bdellovibri
1131	67	6.5	1028	2	Q8BM91	Q8BM91 mus musculu	1204	66.5	6.4	1034	2	Q6N003	Q6N003 homo sapien
1132	67	6.5	1047	1	S8CC_TREPA	O83635 treponema p	1205	66.5	6.4	1073	2	Q7XKJ2	Q7XKJ2 oryza sativ
1133	67	6.5	1075	2	Q7R0Y4	Q7R0Y4 giardia lam	1206	66.5	6.4	1081	2	Q9GNU2	Q9GNU2 paracentrot
1134	67	6.5	1100	2	Q8CIX5	Q8CIX5 mus musculu	1207	66.5	6.4	1445	2	1CN3B_RAT	Q63085 rattus norv
1135	67	6.5	1106	2	Q921J9	Q921J9 mus musculu	1208	66.5	6.4	1445	2	Q24438	Q24438 oryza longi
1136	67	6.5	1106	2	Q64N70	Q64N70 bacteroides	1209	66.5	6.4	1821	1	1LTB2_HUMAN	Q14767 homo sapien
1137	67	6.5	1121	1	DPOL_ADEG1	Q64751 avian adeno	1210	66.5	6.4	1821	2	Q6AZ94	Q6AZ94 homo sapien
1138	67	6.5	1219	2	Q73749	Q73749 xenopus lae	1211	66.5	6.4	1972	1	1P531_HUMAN	Q12888 homo sapien
1139	67	6.5	1255	2	Q6TGL5	Q6TGL5 avian adeno	1212	66.5	6.4	1977	2	Q7Z3U4	Q7Z3U4 homo sapien
1140	67	6.5	1255	2	Q7M5G2	Q7M5G2 avian adeno	1213	66.5	6.4	2077	2	Q9QJ37	Q9QJ37 human herpe
1141	67	6.5	1258	2	Q6PC88	Q6PC88 mus musculu	1214	66.5	6.4	2215	1	1CDN2_DROME	Q9VJB6 drosophila
1142	67	6.5	1389	1	1LTBS_MOUSE	Q8C918 mus musculu	1215	66.5	6.4	2267	2	Q81BX1	Q81BX1 plasmodium
1143	67	6.5	1418	2	Q6A6R7	Q6A6R7 propionibac	1216	66.5	6.4	2871	1	1FBN1_PIG	Q8TV36 sus scrofa
1144	67	6.5	1700	2	Q94GR9	Q94GR9 oryza sativ	1217	66.5	6.4	2974	2	Q815L7	Q815L7 plasmodium
1145	67	6.5	1713	1	1LTBL_MOUSE	Q8CG19 mus musculu	1218	66.5	6.4	3564	1	1CSM1_MOUSE	Q92313 mus musculu
1146	67	6.5	1877	1	1PK5_MOUSE	Q04592 mus musculu	1219	66.5	6.4	6260	2	Q54299	Q54299 streptomyce
1147	67	6.5	2060	2	Q6WZK8	Q6WZK8 homo sapien	1220	66	6.4	87	2	Q63437	Q63437 rattus norv
1148	67	6.5	2811	2	Q68487	Q68487 streptomyce	1221	66	6.4	121	1	1YIPP_DROME	Q9XZF0 drosophila
1149	67	6.5	3396	1	1PGCV_HUMAN	P13611 homo sapien	1222	66	6.4	121	1	1YPL5_CERAE	Q65Z55 cercopitheci
1150	66.5	6.4	148	2	Q73571	Q73571 southern be	1223	66	6.4	121	1	1YPL5_MOUSE	P62699 homo sapien
1151	66.5	6.4	155	2	Q81VK7	Q81VK7 bacillus an	1224	66	6.4	121	1	1YPL5_MOUSE	P62699 homo sapien
1152	66.5	6.4	202	2	Q6ZAF5	Q6ZAF5 oryza sativ	1225	66	6.4	121	2	Q65292	Q65292 mus musculu
1153	66.5	6.4	228	2	Q7TVS8	Q7TVS8 trypanosoma	1226	66	6.4	121	2	Q6DEA6	Q6DEA6 xenopus lae
1154	66.5	6.4	258	1	1UL49_BHV1C	P30022 bovine herp	1227	66	6.4	121	2	Q640U2	Q640U2 xenopus tro
1155	66.5	6.4	258	2	Q77CE3	Q77CE3 bovine herp	1228	66	6.4	123	2	Q80PV3	Q80PV3 porcine rep
1156	66.5	6.4	267	2	Q31201	Q31201 pseudomonas	1229	66	6.4	136	1	1RFOM_METTH	Q27369 methanobact
1157	66.5	6.4	273	2	Q770X9	Q770X9 xenopus lae	1230	66	6.4	172	2	Q8LTL4	Q8LTL4 lactococcus
1158	66.5	6.4	276	2	Q6P5A6	Q6P5A6 homo sapien	1231	66	6.4	177	2	Q6DF17	Q6DF17 xenopus tro
1159	66.5	6.4	281	2	Q7VVI0	Q7VVI0 trypanosoma	1232	66	6.4	184	2	Q8ZY02	Q8ZY02 pyrobaculum
1160	66.5	6.4	293	2	Q885H5	Q885H5 pseudomonas	1233	66	6.4	184	2	Q8ZY02	Q8ZY02 pyrobaculum
1161	66.5	6.4	302	2	Q9VVF5	Q9VVF5 drosophila	1234	66	6.4	194	1	1CSR3_RAT	P50463 rattus norv
1162	66.5	6.4	306	1	1UNG_MOUSE	P97931 mus musculu	1235	66	6.4	198	2	Q71DC4	Q71DC4 drosophila
1163	66.5	6.4	329	2	Q9J1W8	Q9J1W8 mus musculu	1236	66	6.4	202	1	1NF3_RHOPR	Q94733 rhodnius pr
1164	66.5	6.4	340	1	Q74PL5	Q74PL5 geobacter s	1237	66	6.4	243	2	Q62079	Q62079 mus musculu
1165	66.5	6.4	340	1	YD50_MYCTU	P64831 mycobacteri	1238	66	6.4	253	2	Q74DY7	Q74DY7 geobacter s
1166	66.5	6.4	356	2	Q63ZM9	P64832 mycobacteri	1239	66	6.4	265	2	Q92VM3	Q92VM3 rhizobium m
1167	66.5	6.4	357	2	Q6ANR1	Q6ANR1 desulfotale	1240	66	6.4	267	2	Q88D00	Q88D00 pseudomonas
1168	66.5	6.4	361	2	Q6YSY6	Q6YSY6 oryza sativ	1241	66	6.4	273	2	Q66TN8	Q66TN8 solanum tub
1169	66.5	6.4	366	2	Q9BU38	Q9BU38 homo sapien	1242	66	6.4	285	2	Q802T3	Q82A80 streptomyce
1170	66.5	6.4	386	2	Q6XK88	Q6XK88 oryza sativ	1243	66	6.4	276	2	Q82A80	Q82A80 streptomyce
1171	66.5	6.4	405	2	Q7XU17	Q7XU17 oryza sativ	1244	66	6.4	291	1	1NANK_SHIFL	P59437 shigella fl
1172	66.5	6.4	405	2	Q9X0D4	Q9X0D4 thermotoga	1245	66	6.4	320	2	Q7SYN4	Q7SYN4 brachydanio
1173	66.5	6.4	415	2	Q81P11	Q81P11 drosophila	1246	66	6.4	325	2	Q6Z512	Q6Z512 oryza sativ
1174	66.5	6.4	437	1	1SH_RAT	Q91VR2 rattus norv	1247	66	6.4	339	2	Q24698	Q24698 dugesia tig
1175	66.5	6.4	442	2	Q91VR2	Q91VR2 arabidopsis	1248	66	6.4	339	2	Q24700	Q24700 dugesia tig
1176	66.5	6.4	471	2	Q09534	Q09534 caenorhabdi	1249	66	6.4	341	2	Q91XD2	Q91XD2 mus musculu
1177	66.5	6.4	471	2	Q09534	Q09534 mycoplasma	1250	66	6.4	354	2	Q7MUG3	Q7MUG3 porphyromon
1178	66.5	6.4	486	2	Q8RLX9	Q8RLX9 antirrhinum	1251	66	6.4	355	2	Q8BW39	Q8BW39 mus musculu
1179	66.5	6.4	489	2	Q09MRV9	Q09MRV9 antirrhinum	1252	66	6.4	359	1	1LUXA_PHOIL	Q7A575 photorhabdu
1180	66.5	6.4	491	2	Q06324	Q06324 saccharomyc	1253	66	6.4	359	2	Q93CP4	Q93CP4 photorhabdu
1181	66.5	6.4	496	2	P93369	P93369 nicotiana t	1254	66	6.4	382	2	Q57522	Q57522 xenopus lae
1182	66.5	6.4	540	2	Q714U3	Q714U3 haemophilu	1255	66	6.4	390	2	Q721C1	Q721C1 plasmodium
1183	66.5	6.4	569	2	Q9H9S6	Q9H9S6 homo sapien	1256	66	6.4	397	2	Q8N6G7	Q8N6G7 homo sapien
1184	66.5	6.4	578	2	Q904P4	Q904P4 drosophila	1257	66	6.4	402	2	Q7T121	Q7T121 brachydanio
1185	66.5	6.4	586	2	Q7NNX7	Q64N89 bacteroides	1258	66	6.4	410	2	Q9P868	Q9P868 piromyces e
1186	66.5	6.4	586	2	Q7NNX7	Q7NNX7 gloeobacter	1259	66	6.4	423	2	Q9F156	Q9F156 rhodobacter
1187	66.5	6.4	588	2	Q661Q2	Q661Q2 xenopus lae	1260	66	6.4	445	2	Q6RF54	Q6RF54 rhodobacter
1188	66.5	6.4	607	2	Q7Q1T5	Q7Q1T5 anopheles g	1261	66	6.4	451	1	1Z222_HUMAN	Q9UK12 homo sapien
1189	66.5	6.4	608	2	Q6A782	Q6A782 propionibac	1262	66	6.4	451	2	Q9P1U5	Q9P1U5 homo sapien
1190	66.5	6.4	608	2	Q6A782	Q6A782 propionibac	1263	66	6.4	454	2	Q8BIS1	Q8BIS1 mus musculu
1191	66.5	6.4	615	2	Q7Q9V5	Q7Q9V5 homo sapien	1264	66	6.4	460	1	1GUN2_CLOJO	P37701 clostridium
1192	66.5	6.4	628	2	Q7Q9B1	Q7Q9B1 giardia lam	1265	66	6.4	472	2	Q806B9	Q806B9 cercopitheci
1193	66.5	6.4	639	2	Q8TPL3	Q8TPL3 methanosarc	1266	66	6.4	477	2	Q97600	Q97600 cryotolagus
1194	66.5	6.4	671	2	Q8SPD9	Q8SPD9 encephalito	1267	66	6.4	493	1	1AMYR_DROTE	Q76260 drosophila
1195	66.5	6.4	682	2	Q8QS63	Q8QS63 pongine her	1268	66	6.4	505	2	Q8CDD0	Q8CDD0 mus musculu
1196	66.5	6.4	701	1	1UGUG02	Q9UG02 homo sapien	1269	66	6.4	509	2	Q9VIW0	Q9VIW0 drosophila
1197	66.5	6.4	708	1	1HELS_SULSO	Q97VY9 sulfolobus	1270	66	6.4	512	2	Q8OWS0	Q8OWS0 mus musculu
1198	66.5	6.4	752	2	Q81Z99	Q81Z99 homo sapien	1271	66	6.4	528	2	Q9XVL8	Q9XVL8 caenorhabdi
1199	66.5	6.4	768	2	Q8FKS2	Q8FKS2 escherichia	1272	66	6.4	532	2	Q96671	Q96671 drosophila

1273	66	6.4	534	2	Q8Q0X9	Q8c0x9 methanosearc	1346	65.5	6.3	251	2	Q76KS9	Q76ke9 trichomonas
1274	66	6.4	539	2	Q8I957	Q8i957 xenopus lae	1347	65.5	6.3	255	2	Q9DAN2	Q9dan2 mus musculus
1275	66	6.4	543	2	Q9XZC2	Q9xxc2 drosophila	1348	65.5	6.3	261	2	Q943C9	Q943c9 oryza sativ
1276	66	6.4	548	2	Q9DDK9	Q9ddk9 xenopus lae	1349	65.5	6.3	271	2	Q8R3U3	Q8r3u3 mus musculus
1277	66	6.4	553	2	Q9VVV5	Q9vvv5 drosophila	1350	65.5	6.3	272	2	Q661J9	Q661j9 xenopus tro
1278	66	6.4	553	2	Q8BXU0	Q8bxu0 mus musculus	1351	65.5	6.3	277	2	Q40896	Q40896 petunia hyb
1279	66	6.4	562	2	Q8IGS4	Q8igs4 drosophila	1352	65.5	6.3	280	2	Q8XL14	Q8xl14 clostridium
1280	66	6.4	578	2	Q88DK0	Q88dk0 rhizobium l	1353	65.5	6.3	281	2	Q966N5	Q966n5 caenorhabdi
1281	66	6.4	582	1	YMA5_CAEEL	P34450 caenorhabdi	1354	65.5	6.3	286	2	Q932V7	Q932v7 mycoplasma
1282	66	6.4	583	2	Q8BKL7	Q8bkl7 mus musculus	1355	65.5	6.3	298	2	Q9V066	Q9v066 pyrococcus
1283	66	6.4	586	2	Q8X0G2	Q8x0g2 neurospora	1356	65.5	6.3	301	1	VG30_BPPF3	P03626 bacterioph
1284	66	6.4	618	2	Q6ZKX6	Q6zkk6 oryza sativ	1357	65.5	6.3	302	2	Q86Z80	Q86z80 magnaporth
1285	66	6.4	625	2	Q86SV2	Q86sv2 homo sapien	1358	65.5	6.3	318	2	Q8IM23	Q8im23 plasmodium
1286	66	6.4	626	2	Q9CJMO	Q9cjm0 pasteurella	1359	65.5	6.3	323	2	Q7XY80	Q7xy80 griffithaia
1287	66	6.4	637	2	Q7EY96	Q7ey96 oryza sativ	1360	65.5	6.3	326	2	Q78CJ5	Q78cj5 neurospora
1288	66	6.4	669	2	Q8H631	Q8h631 oryza sativ	1361	65.5	6.3	360	2	Q6HP72	Q6hp72 bacillus th
1289	66	6.4	673	1	FXO3_HUMAN	Q43524 homo sapien	1362	65.5	6.3	369	2	Q8T5G1	Q8t5g1 trichomonas
1290	66	6.4	683	2	Q6FXI0	Q6fxi0 candida gla	1363	65.5	6.3	369	2	Q8T5G2	Q8t5g2 trichomonas
1291	66	6.4	689	2	Q9JKU4	Q9jku4 mus musculus	1364	65.5	6.3	370	1	COMM_DROME	Q24139 drosophila
1292	66	6.4	694	2	Q8YKX5	Q8yxk5 oryza sativ	1365	65.5	6.3	385	2	Q69JB8	Q69jb8 oryza sativ
1293	66	6.4	704	2	Q8PC08	Q8pc08 brachydanio	1366	65.5	6.3	388	2	Q800R3	Q800r3 gallus gall
1294	66	6.4	710	2	Q8PB38	Q8pb38 mus musculus	1367	65.5	6.3	399	2	Q9CUC2	Q9cuc2 mus musculus
1295	66	6.4	711	2	Q8BQC8	Q8bqc8 mus musculus	1368	65.5	6.3	405	2	Q6L4B5	Q6l4b5 solanum dem
1296	66	6.4	744	2	Q8CYJ7	Q8cyj7 erwinia car	1369	65.5	6.3	408	2	Q7PRS9	Q7pr9 anopheles g
1297	66	6.4	751	1	SM3C_HUMAN	Q95985 homo sapien	1370	65.5	6.3	411	2	Q7PY76	Q7py76 anopheles g
1298	66	6.4	756	2	Q8Y4V2	Q8y4v2 bovine vira	1371	65.5	6.3	430	2	Q7XL65	Q7xl65 oryza sativ
1299	66	6.4	757	2	Q8MJ24	Q8mj24 bos taurus	1372	65.5	6.3	437	2	Q9QM71	Q9qm71 fowl adenov
1300	66	6.4	763	2	Q9LM99	Q9lm99 arabidopsis	1373	65.5	6.3	444	2	Q6DDV2	Q6ddv2 xenopus lae
1301	66	6.4	805	1	GYRB_CHLPN	Q9z8r3 chlamydia p	1374	65.5	6.3	470	2	Q7ROX4	Q7rox4 giardia lam
1302	66	6.4	873	2	Q9XSR1	Q9xsr1 canis famil	1375	65.5	6.3	471	2	Q9AK04	Q9ak04 streptomyce
1303	66	6.4	889	2	Q745A6	Q745a6 mycobacteri	1376	65.5	6.3	502	2	Q8R5B3	Q8r5b3 mus musculus
1304	66	6.4	952	2	Q7PZ16	Q7pzi6 anopheles g	1377	65.5	6.3	508	2	Q7TPB2	Q7tpb2 mus musculus
1305	66	6.4	964	2	Q9NV77	Q9nv77 homo sapien	1378	65.5	6.3	513	1	RFP_HUMAN	P14373 homo sapien
1306	66	6.4	1008	2	Q9FFP8	Q9fpp8 arabidopsis	1379	65.5	6.3	513	1	RFP_MOUSE	Q62158 mus musculus
1307	66	6.4	1045	2	Q9NV01	Q9nbv1 arabidopsis	1380	65.5	6.3	514	2	Q6LFT21	Q6lt21 photobacter
1308	66	6.4	1063	2	Q7SB04	Q7sb04 neurospora	1381	65.5	6.3	528	2	Q8R2M7	Q8r2m7 mus musculus
1309	66	6.4	1121	2	Q8IW09	Q8iw09 homo sapien	1382	65.5	6.3	530	2	Q6BQF8	Q6bqf8 debaryomyce
1310	66	6.4	1184	2	Q86V58	Q86v58 homo sapien	1383	65.5	6.3	547	2	Q6MRP6	Q6mrp6 bdellovibri
1311	66	6.4	1186	2	Q86V58	Q86v58 homo sapien	1384	65.5	6.3	556	2	Q7M5G9	Q7m5g9 fowl adenov
1312	66	6.4	1224	2	Q00533	O00533 homo sapien	1385	65.5	6.3	573	2	Q68MR2	Q68mr2 homo sapien
1313	66	6.4	1342	1	Z335_HUMAN	Q9h4z2 homo sapien	1386	65.5	6.3	586	2	Q37867	Q37867 bacterioph
1314	66	6.4	1396	1	VCAP_VZVD	P09245 varicella-z	1387	65.5	6.3	589	2	Q9GTP2	Q9gtp2 trichomonas
1315	66	6.4	1396	2	QCQCT5	Q6qcl5 human herpe	1388	65.5	6.3	603	2	Q7QGJ5	Q7qgj5 anopheles g
1316	66	6.4	1620	1	PCX3_MOUSE	Q6v159 mus musculus	1389	65.5	6.3	604	2	Q6NSS3	Q6nsa3 mus musculus
1317	66	6.4	1693	2	Q8FLF9	Q6flf9 candida gla	1390	65.5	6.3	605	1	WIS1_SCHPO	P33886 schizosacch
1318	66	6.4	1769	2	Q9P273	Q9p273 homo sapien	1391	65.5	6.3	605	2	Q7XR71	Q7xr71 oryza sativ
1319	66	6.4	1828	2	Q86TD2	Q86td2 mus musculus	1392	65.5	6.3	609	2	Q9NZX7	Q9nzx7 homo sapien
1320	66	6.4	1918	2	Q86AS3	Q86as3 dictyosteli	1393	65.5	6.3	622	1	ESR1_ONCMY	P16058 oncorhynch
1321	66	6.4	1979	2	Q88196	Q88196 mus musculus	1394	65.5	6.3	629	2	Q7RWM5	Q7rwm5 neurospora
1322	66	6.4	1995	2	Q7QJ88	Q7qj88 anopheles g	1395	65.5	6.3	635	2	Q6AHQ4	Q6ahq4 caenorhabdi
1323	66	6.4	2193	2	Q6S5G1	Q6s5g1 human enter	1396	65.5	6.3	656	1	CGBP_HUMAN	Q6c7d6 yarrowia li
1324	66	6.4	2193	2	Q6DHE1	Q9dhe1 mus musculus	1397	65.5	6.3	656	1	CAOI_PHACI	Q9p0u4 homo sapien
1325	66	6.4	2346	2	Q9JLC1	Q9jlc1 mus musculus	1398	65.5	6.3	661	1	Q9LJQ7	Q9hy18 phascolarct
1326	66	6.4	2715	2	Q9WTS6	Q9wts6 mus musculus	1399	65.5	6.3	666	2	Q9LJQ7	Q9ljq7 arabidopsis
1327	66	6.4	3005	1	ZFH2_DROME	P28167 drosophila	1400	65.5	6.3	677	2	Q9XDT1	Q9xdt1 bacillus sp
1328	66	6.4	3106	1	LMA2_MOUSE	Q6o675 mus musculus	1401	65.5	6.3	682	2	Q8P920	Q8p920 xanthomonas
1329	66	6.4	328	2	Q6C9E2	Q6c9e2 yarrowia li	1402	65.5	6.3	690	2	Q7UUC2	Q7uuc2 rhodopirell
1330	65.5	6.3	156	2	Q6CKD4	Q6ckd4 paracoccidi	1403	65.5	6.3	690	2	Q8QFT7	Q8qfc7 fugu rubrip
1331	65.5	6.3	177	1	NRFH_WOLSU	Q74be5 wolinnella s	1404	65.5	6.3	701	2	FBL1_MOUSE	Q88r79 mus musculus
1332	65.5	6.3	197	2	Q74BE5	Q74be5 geobacter s	1405	65.5	6.3	705	1	Q91XV1	Q91xv1 rattus norv
1333	65.5	6.3	202	2	Q95VR2	Q95vr2 dilocarcinu	1406	65.5	6.3	708	2	Q19718	Q19718 caenorhabdi
1334	65.5	6.3	211	2	Q94H14	Q94h14 oryza sativ	1407	65.5	6.3	732	2	Q8VQM5	Q8vqm5 klebsiella
1335	65.5	6.3	211	2	Q7XGS7	Q7xgs7 oryza sativ	1408	65.5	6.3	747	1	PKP1_HUMAN	Q13835 homo sapien
1336	65.5	6.3	216	2	Q6B341	Q6b341 mariniibacil	1409	65.5	6.3	794	1	ZB17_MOUSE	Q60821 mus musculus
1337	65.5	6.3	218	1	KAD_BORR	Q7wku8 bordetella	1410	65.5	6.3	817	2	Q9V461	Q9v461 drosophila
1338	65.5	6.3	218	1	KAD_BORR	Q7w7g0 bordetella	1411	65.5	6.3	817	2	Q9V461	Q9v461 drosophila
1339	65.5	6.3	218	1	KAD_BORPE	P39068 bordetella	1412	65.5	6.3	825	2	Q46652	Q46652 papio anubi
1340	65.5	6.3	221	1	RUV_CORGL	Q9ae11 corynebacte	1413	65.5	6.3	829	2	Q39233	Q39233 thesus monk
1341	65.5	6.3	221	1	RUV_CORGL	Q9ae11 corynebacte	1414	65.5	6.3	829	2	Q9J2M4	Q9j2m4 thesus monk
1342	65.5	6.3	229	2	Q8N2M4	Q8n2m4 homo sapien	1415	65.5	6.3	851	2	Q63ZY3	Q63zy3 homo sapien
1343	65.5	6.3	232	2	Q66PV2	Q66pv2 acropora mi	1416	65.5	6.3	859	2	Q6GUF5	Q6gu5 homo sapien
1344	65.5	6.3	234	1	UREA_HELHE	P42822 helicobacte	1417	65.5	6.3	876	2	Q9P210	Q9p210 homo sapien
1345	65.5	6.3	235	2	Q9LWA5	Q9lwa5 medicago sa	1418	65.5	6.3	891	2	Q9VV38	Q9vv38 drosophila

1419	65.5	6.3	903	2	Q9UV99	Q9UV99 neurospora	1492	65	6.3	275	2	Q84DK1	Q84dk1 listeria se
1420	65.5	6.3	934	2	Q7UZE0	Q7UZE0 rhodospirell	1493	65	6.3	275	2	Q8XYI1	Q8xyi1 ralstonia s
1421	65.5	6.3	955	2	Q9N600	Q9N600 leptonotars	1494	65	6.3	278	2	Q82J43	Q82j43 streptomyce
1422	65.5	6.3	956	2	Q70KL5	Q70KL5 tuber borch	1495	65	6.3	288	2	Q8ABM7	Q8abm7 bacteroides
1423	65.5	6.3	959	2	Q6PUA9	Q6PUA9 ambystoma s	1496	65	6.3	292	2	Q6C561	Q6c561 yarrowia li
1424	65.5	6.3	1002	1	RP01_NICSY	Q93Y94 nicotiana s	1497	65	6.3	293	2	Q7UMS9	Q7ums9 rhodospirell
1425	65.5	6.3	1010	2	Q45247	Q45247 caenorhabdi	1498	65	6.3	301	2	Q8YRV1	Q8yrv1 anabaena sp
1426	65.5	6.3	1020	2	Q9L3L4	Q9L3L4 bifidobacte	1499	65	6.3	304	2	Q92IU4	Q92iu4 mus musculu
1427	65.5	6.3	1043	2	Q6NXZ1	Q6NXZ1 mus musculu	1500	65	6.3	310	2	Q8TPK4	Q8tpk4 methanosarc
1428	65.5	6.3	1076	2	Q943E4	Q943E4 oryza sativ							
1429	65.5	6.3	1239	2	Q75LL9	Q75LL9 oryza sativ							
1430	65.5	6.3	1287	2	Q872W7	Q872W7 neurospora							
1431	65.5	6.3	1302	2	Q8K083	Q8K083 m zfp536 pr							
1432	65.5	6.3	1317	2	Q6IQ50	Q6IQ50 homo sapien							
1433	65.5	6.3	1320	2	Q64FY2	Q64FY2 homo sapien							
1434	65.5	6.3	1353	2	Q7RYF4	Q7RYF4 neurospora							
1435	65.5	6.3	1358	2	Q64FX7	Q64FX7 homo sapien							
1436	65.5	6.3	1364	2	Q64FY1	Q64FY1 homo sapien							
1437	65.5	6.3	1365	2	Q75N88	Q75N88 homo sapien							
1438	65.5	6.3	1378	2	Q6L138	Q6L138 mus musculu							
1439	65.5	6.3	1416	2	Q9VYMI	Q9VYMI drosophila							
1440	65.5	6.3	1417	2	Q8X6G3	Q8X6G3 escherichia							
1441	65.5	6.3	1439	2	Q64FX8	Q64FX8 homo sapien							
1442	65.5	6.3	1466	2	Q42930	Q42930 schizosacch							
1443	65.5	6.3	1495	2	Q62NL2	Q62NL2 homo sapien							
1444	65.5	6.3	1571	2	Q54978	Q54978 mus musculu							
1445	65.5	6.3	1572	2	Q8F5N0	Q8F5N0 mus musculu							
1446	65.5	6.3	1617	2	Q80U47	Q80U47 mus musculu							
1447	65.5	6.3	1633	2	Q8CMP4	Q8CMP4 staphylococ							
1448	65.5	6.3	1824	2	Q6DRL4	Q6DRL4 brachydanio							
1449	65.5	6.3	1989	1	SL2B_HUMAN	Q8NEV8 homo sapien							
1450	65.5	6.3	2219	2	Q95MJ4	Q95MJ4 myotis luci							
1451	65.5	6.3	2327	2	Q91BG7	Q91BG7 xenopus lae							
1452	65.5	6.3	2328	2	Q95MI9	Q95MI9 erinaceus e							
1453	65.5	6.3	2471	1	NTC2_HUMAN	Q04721 homo sapien							
1454	65.5	6.3	2871	1	FBN1_HUMAN	P35555 homo sapien							
1455	65.5	6.3	2871	1	Q75N87	Q75N87 homo sapien							
1456	65.5	6.3	2872	2	Q9WU88	Q9WU88 rattus norv							
1457	65.5	6.3	3672	1	LMJ2_CABEL	Q21313 caenorhabdi							
1458	65.5	6.3	3704	2	Q91904	Q91904 caenorhabdi							
1459	65.5	6.3	3950	2	Q7YRF5	Q7YRF5 canis famli							
1460	65.5	6.3	5604	2	Q8WZ53	Q8WZ53 homo sapien							
1461	65.5	6.3	6684	1	R1AB_CVPPU	Q91W06 p replicase							
1462	65	6.3	108	2	Q8PS65	Q8PS65 methanosarc							
1463	65	6.3	122	1	YCS5_YEAST	P37264 saccharomyc							
1464	65	6.3	122	2	Q8NIN3	Q8NIN3 saccharomyc							
1465	65	6.3	127	2	Q6CFZ9	Q6CFZ9 yarrowia li							
1466	65	6.3	130	2	Q7OKA7	Q7OKA7 anopheles g							
1467	65	6.3	147	2	Q05418	Q05418 saccharomyc							
1468	65	6.3	148	2	Q8N7B4	Q8N7B4 homo sapien							
1469	65	6.3	149	2	Q8RV68	Q8RV68 arabidopsis							
1470	65	6.3	149	2	Q8VQH3	Q8VQH3 uncultured							
1471	65	6.3	155	2	Q6QMT3	Q6QMT3 mus musculu							
1472	65	6.3	160	2	Q8KJ04	Q8KJ04 helicobacte							
1473	65	6.3	176	2	Q8KIZ2	Q8KIZ2 helicobacte							
1474	65	6.3	178	2	Q6TPN5	Q6TPN5 newcastle d							
1475	65	6.3	182	1	YN66_HALN1	Q9HNV9 halobacteri							
1476	65	6.3	192	2	Q6NZV4	Q6NZV4 brachydanio							
1477	65	6.3	197	2	Q7QPT2	Q7QPT2 giardia lam							
1478	65	6.3	200	2	Q65926	Q65926 human coxae							
1479	65	6.3	201	2	Q8ZBR5	Q8ZBR5 yersinia pe							
1480	65	6.3	202	2	Q77000	Q77000 rhodnius pr							
1481	65	6.3	202	2	Q7TY55	Q7TY55 rhodnius pr							
1482	65	6.3	213	2	Q7PTI9	Q7PTI9 anopheles g							
1483	65	6.3	215	2	Q9SN24	Q9SN24 arabidopsis							
1484	65	6.3	216	1	KAD_LACPL	Q88XW5 lactobacill							
1485	65	6.3	223	2	Q9VGW0	Q9VGW0 drosophila							
1486	65	6.3	244	2	Q86XL8	Q86XL8 homo sapien							
1487	65	6.3	246	2	Q85307	Q85307 cowpox viru							
1488	65	6.3	249	2	Q7QEV2	Q7QEV2 anopheles g							
1489	65	6.3	256	2	Q7NQR8	Q7NQR8 chromobacte							
1490	65	6.3	264	2	Q8PVW8	Q8PVW8 methanosarc							
1491	65	6.3	267	2	Q82174	Q82174 streptomyce							

ALIGNMENTS

RESULT 1

Q6UXS2	PRELIMINARY;	PRT;	192 AA.
ID	Q6UXS2		
AC	Q6UXS2;		
DT	05-JUL-2004 (TREMBlrel. 27, Created)		
DT	05-JUL-2004 (TREMBlrel. 27, Last sequence update)		
DT	05-JUL-2004 (TREMBlrel. 27, Last annotation update)		
DE	SPR1965=UNQ1965;		
GN	ORFNames=UNQ1965;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;		
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,		
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,		
RA	Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,		
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,		
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,		
RA	Seshagiri S., Stambos L., Singh J., Smith V., Stinson J., Vegts A.,		
RA	Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.H., Yansura D.,		
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,		
RA	Godowski P.;		
RT	"The secreted protein discovery initiative (SPDI), a large-scale		
RT	effort to identify novel human secreted and transmembrane proteins: a		
RT	bioinformatics assessment."		
RL	Genome Res. 13:2265-2270 (2003).		
DR	EMBL; AY358229; AAQ88596.1; -.		
DR	InterPro; IPR002579; MsrB.		
DR	InterPro; IPR011057; Msr4_like.		
DR	Pfam; PF01641; SeIR; 1.		
DR	ProDom; PD004057; DUF25; 1.		
DR	TIGRFAMs; TIGR00357; DUF25; 1.		
SQ	SEQUENCE 192 AA; 20702 MW; C3326F6103369083 CRC64;		

Query Match 100.0%; Score 1036; DB 2; Length 192;

Best Local Similarity 100.0%; Pred. No. 6.4e-90; Mismatches 0; Indels 0; Gaps 0;

Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPRTLPRPLSLCLSLCLCLCLAAALGSAQSGCRDKKCKVFSQQELRRLTFLQYH 60

Db 1 MSPRTLPRPLSLCLSLCLCLCLAAALGSAQSGCRDKKCKVFSQQELRRLTFLQYH 60

QY 61 VTQKGTSAFEGEYTHHKDPGIYKVCVCGTLPFKSETKFDGSGGWPSPHVDINSEATTF 120

Db 61 VTQKGTSAFEGEYTHHKDPGIYKVCVCGTLPFKSETKFDGSGGWPSPHVDINSEATTF 120

QY 121 TDDFSYGHVRVETSCQCGAHLGHIFDDGPRPTGKRYCINSALSFPTADSSGTAGGSG 180

Db 121 TDDFSYGHVRVETSCQCGAHLGHIFDDGPRPTGKRYCINSALSFPTADSSGTAGGSG 180

QY 181 VASPAQADKAE 192

Db 181 VASPAQADKAE 192

RESULT 2

```
Q8IXL7
ID Q8IXL7 PRELIMINARY; PRT; 185 AA.
AC Q8IXL7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE LOC253827 protein.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus J., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RA Strausberg R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC040053; AAH40053.1; -.
DR HSSP; P14930; 1L1D.
DR InterPro; IPR002579; MsrB.
DR InterPro; IPR011057; Msr4_like.
DR Pfam; PF01641; SelR; 1.
DR ProDom; PD004057; DUF25; 1.
DR TIGRFAMs; TIGR00357; DUF25; 1.
SQ SEQUENCE 185 AA; 20010 MW; 37576AFCF88CE227 CRC64;

Query Match 84.5%; Score 875; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.1e-74;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 SGSCRDKNKCVFQQELRLKRLTLPQYHVTQKGTSAFGEYTHHKDPGIYKCVCGT 91
Db 25 SGSCRDKNKCVFQQELRLKRLTLPQYHVTQKGTSAFGEYTHHKDPGIYKCVCGT 84
QY 92 PLFKSETKFDGSGWPSFDHVINSEAITFTDDFSYGMHVRVETSCSCGAHLGHIFDDGPR 151
Db 85 PLFKSETKFDGSGWPSFDHVINSEAITFTDDFSYGMHVRVETSCSCGAHLGHIFDDGPR 144
QY 152 PTGKRYCINSAALSTPADSSGTARGSGVSPQAQDAKEL 192
Db 145 PTGKRYCINSAALSTPADSSGTARGSGVSPQAQDAKEL 185

RESULT 3
Q8BU85
ID Q8BU85 PRELIMINARY; PRT; 186 AA.
AC Q8BU85;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
```

DE Mus musculus 0 day neonate lung cDNA, RIKEN full-length enriched library, clone:E030016P18 product:weakly similar to TRANSCRIPTIONAL REGULATOR.

DE GN Name=D430026P16Rik;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Lung;

RX STRAIN=C57BL/6J; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; MEDLINE=99279253;

RA Carninci P., Hayashizaki Y.;

RT "High-efficiency full-length cDNA cloning.";

RL Meth. Enzymol. 303:19-44 (1999).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Lung;

RX STRAIN=C57BL/6J; PubMed=11217851; DOI=10.1038/35055500; MEDLINE=21085660;

RA RIKEN FANTOM Consortium;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690 (2001).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Lung;

RX STRAIN=C57BL/6J; PubMed=11042159; DOI=10.1101/gr.145100; MEDLINE=20499374;

RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";

RL Genome Res. 10:1617-1630 (2000).

RN [5]

RP SEQUENCE FROM N.A.

RC TISSUE=Lung;

RX STRAIN=C57BL/6J; PubMed=11076861; DOI=10.1101/gr.152600; MEDLINE=20530913;

RA Shibata K., Itoh M., Aizawa K., Nagao K., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";

RL Genome Res. 10:1757-1771 (2000).

RN [6]

RP SEQUENCE FROM N.A.

RC TISSUE=Lung;

RX STRAIN=C57BL/6J; PubMed=11076861; DOI=10.1101/gr.152600; MEDLINE=20530913;

RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK086975; BAC39776.1; -.
DR HSSP; P14930; 1L1D.
DR MGD; MGI:2443538; D430026P16Rik.
DR InterPro; IPR002579; MsrB.
DR InterPro; IPR011057; Msr4_like.


```

DR Pfam: PF01641; SelR: 1.
DR ProDom: PD004057; DUF25; 1.
DR TIGRFAMs: TIGR00357; DUF25; 1.
SQ SEQUENCE 186 AA; 20224 MW; 9592DAE8F862A1F CRC64;

Query Match 76.6%; Score 793.5; DB 2; Length 186;
Best Local Similarity 91.5%; Pred. No. 5.4e-67;
Matches: 150; Conservative 5; Mismatches 4; Indels 5; Gaps 3;

QY 32 SGSCRDKNCKVFSQQLRLKRLTPLYHVTOEKGTSAFGEYTHHKDPGIYKCVCGT 91
DB 25 SGSCRDKNCKVFSQQLRLKRLTPLYHVTOEKGTSAFGEYTHHKDPGIYKCVCGT 84

QY 92 PLFKSETKFDGSGWPSFHDVINSALITFTDDFSYGMHVRVETSCQCGAHLGHIFDDGPR 151
DB 85 PLFKSETKFDGSGWPSFHDVINSALITFTDDFSYGMHVRVETSCQCGAHLGHIFDDGPR 144

QY 152 PTGKRYCINSALSTPTPADSSGTAEAGSGV---ASPAQADKAE 192
DB 145 PTGKRYCINSALSTPTPADSS-EAE-GSGIKESGSPAADRAEL 186

RESULT 4
Q61Q80 PRELIMINARY; PRT; 186 AA.
AC Q61Q80;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Zgc:86909.
CN ORFName=zgc:86909;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smalios D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC071530; AAH71530.1; -.
DR ZFIN; ZDB-GENE-040625-74; zgc:86909.
DR InterPro; IPR002579; MsrB.
DR ProDom; PD004057; DUF25; 1.
DR TIGRFAMs; TIGR00357; DUF25; 1.
SQ SEQUENCE 186 AA; 20482 MW; 67CB895BAF9DD1B9 CRC64;

Query Match 57.7%; Score 598; DB 2; Length 186;
Best Local Similarity 68.1%; Pred. No. 1.7e-48;
Matches: 109; Conservative 16; Mismatches 35; Indels 0; Gaps 0;

QY 32 SGSCRDKNCKVFSQQLRLKRLTPLYHVTOEKGTSAFGEYTHHKDPGIYKCVCGT 91
DB 25 SGTCSRKKTWPKTFPEBELKRLTPLYHVTOEKGTSAFGEYTHHKDPGIYKCVCGT 84

QY 92 PLFKSETKFDGSGWPSFHDVINSALITFTDDFSYGMHVRVETSCQCGAHLGHIFDDGPR 151
DB 85 PLFKSETKFDGSGWPSFHDVINSALITFTDDFSYGMHVRVETSCQCGAHLGHIFDDGPR 144

QY 152 PTGKRYCINSALSTPTPADSSGTAEAGSGV---ASPAQADKAE 191
DB 145 PTGKRYCINSALSTPTPADSS-EAE-GSGIKESGSPAADRAEL 184

RESULT 5
MSRB_SALTI STANDARD; PRT; 137 AA.
AC P65450; Q8XGD3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Peptide methionine sulfoxide reductase msrB (EC 1.8.4.6).
CN Name=msrB; OrderedLocusName=STY1824, t1170;
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18."
RL Nature 413:848-852(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
DOI=10.1128/JB.185.7.2330-2337.2003;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.P., Rose D.J.,
RA Burland V., Kodoyanni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18."
RL J. Bacteriol. 185:2330-2337(2003).
CC -|- CATALYTIC ACTIVITY: Protein L-methionine + thioredoxin disulfide =
CC Protein L-methionine S-oxide + thioredoxin.
CC -|- SIMILARITY: Belongs to the msrB thio sulfoxide reductase family.
CC
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CC
CC EMBL; AL627271; CAD02063.1; ALT_INIT.
CC EMBL; AE016838; AAC68827.1; ALT_INIT.
CC HSSP; P14930; ILID.
CC HAMAP; MF_01400; -.
CC InterPro; IPR002579; DUF25.

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DR InterPro; IPR011057; Mss4_like.
DR Pfam; PF01641; SelR; 1.
DR ProDom; PD004057; DUF25; 1.
DR TIGRFAMs; TIGR00357; DUF25; 1.
KW Complete proteome; Oxidoreductase.
FT ACT_SITE 118 By similarity.
SQ SEQUENCE 137 AA; 15471 MW; 90F79ABD5B4283CF CRC64;

Query Match 41.2%; Score 427; DB 1; Length 137;
Best Local Similarity 53.8%; Pred. No. 1.8e-32;
Matches 71; Conservative 27; Mismatches 34; Indels 0; Gaps 0;

QY 46 SQQLRKLPLQVHYVTOEKGTSAPEGEYTHHKDPGIYKVCVCGTLPFKSETKFDGSGG 105
DB 6 SABELKKLSLSEMOFYVTDGRTGTEPPFTGRLLHNKRDGVYHCLVCDTLPFHSHTKYDSCGC 65
QY 106 WPSFHDVINSRAITFTDDFSYGMHVRVETSCSQCAHLGHIFFDGPRTGKRYCINSAA 165
DB 66 WPSFYQPVSEAIRYIDDFSHGMQVRVIRCGNCDALHGHVFPDGPQPTGERYCVNSASLA 125
QY 166 FTPADSSGTABG 177
DB 126 FSDEKNGDQLKG 137

RESULT 6
MSRB SALTY STANDARD; PRT; 137 AA.
AC P65449; O8XGD3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Peptide methionine sulfoxide reductase msrB (EC 1.8.4.6).
GN Name=msrB; OrderedLocNames=STM1291;
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=LT2 / SGSC1412 / ATCC 700720;
RA MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RA "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2.";
RL Nature 413:852-856(2001).
CC -!- CATALYTIC ACTIVITY: Protein L-methionine + thioredoxin disulfide =
protein L-methionine S-oxide + thioredoxin.
CC -!- SIMILARITY: Belongs to the msrB Met sulfoxide reductase family.
CC
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CC or send an email to license@ebi-sib.ch).
CC
CC -----
DR EMBL; AE008756; AAL20216.1; ALT_INIT.
DR HSSP; P14930; IL1D.
DR StyGene; SG????; msrB.
DR HAMAP; MF 01400; -; 1.
DR InterPro; IPR002579; DUF25.
DR InterPro; IPR011057; Mss4_like.
DR Pfam; PF01641; SelR; 1.
DR ProDom; PD004057; DUF25; 1.
DR TIGRFAMs; TIGR00357; DUF25; 1.
KW Complete proteome; Oxidoreductase.
FT ACT_SITE 118 By similarity.
SQ SEQUENCE 137 AA; 15471 MW; 90F79ABD5B4283CF CRC64;

Query Match 41.2%; Score 427; DB 1; Length 137;
Best Local Similarity 53.8%; Pred. No. 1.8e-32;
Matches 71; Conservative 27; Mismatches 34; Indels 0; Gaps 0;

QY 46 SQQLRKLPLQVHYVTOEKGTSAPEGEYTHHKDPGIYKVCVCGTLPFKSETKFDGSGG 105
DB 6 SABELKKLSLSEMOFYVTDGRTGTEPPFTGRLLHNKRDGVYHCLVCDTLPFHSHTKYDSCGC 65
QY 106 WPSFHDVINSRAITFTDDFSYGMHVRVETSCSQCAHLGHIFFDGPRTGKRYCINSAA 165
DB 66 WPSFYQPVSEAIRYIDDFSHGMQVRVIRCGNCDALHGHVFPDGPQPTGERYCVNSASLA 125
QY 166 FTPADSSGTABG 177
DB 126 FSDEKNGDQLKG 137

RESULT 7
Q9CBM2 PRELIMINARY; PRT; 202 AA.
AC Q9CBM2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transcriptional regulator, putative; 35498-34111.
GN Name=F22G10.17;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
RA Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Fraser C.M.;
RA Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Town C.D., Kaul S.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC024260; AAC51964.1; -.
DR PIR; H96576; H96576.
DR HSSP; P14930; IL1D.
DR InterPro; IPR002579; MsrB.
DR InterPro; IPR011057; Mss4_like.
DR Pfam; PF01641; SelR; 1.
DR ProDom; PD004057; DUF25; 1.
DR TIGRFAMs; TIGR00357; DUF25; 1.
SQ SEQUENCE 202 AA; 22607 MW; DBF2554E14511B6C CRC64;

Query Match 40.8%; Score 423; DB 2; Length 202;
Best Local Similarity 48.6%; Pred. No. 6.9e-32;
Matches 84; Conservative 25; Mismatches 52; Indels 12; Gaps 2;

QY 5 RTLPRLSLCLSLCLCLALAAAGSAQSGCRD-----KKNCKVVFQQBLRKLTLPLY 59
DB 35 RSLSKPRLNLSLV-----YSMGSSSSSPKPNVQAEKNEFASLSENEWKKRLTPEQY 87
QY 60 HVTQEKGTSAPEGEYTHHKDPGIYKVCVCGTLPFKSETKFDGSGGSPFDVINSRAIT 119
DB 88 YITRQKGTERTAFTEGYWNSKTPGVYNCVCCDTLPFDSSSTKFDGSGTPSPSYQPIGNVKT 147
QY 120 FTDDFSYGMHVRVETSCSQCAHLGHIFFDGPRTGKRYCINSAA 172
DB 148 KLDSLIFMPRQEVVCAVCAHGHVFPDGPRTGKRYCINSAA 200

RESULT 8
Q8TTI4 PRELIMINARY; PRT; 147 AA.
ID Q8TTI4
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AC	Q8T14;	
DT	01-JUN-2002 (TrEMBLrel. 21, Created)	
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)	
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)	
DE	Pilin-like transcription factor.	
GN	OrderedLocusNames=MA0449;	
OS	Methanosarcina acetivorans.	
OC	Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;	
OC	Methanosarcinaceae; Methanosarcina.	
OX	NCBI_TaxID=2214;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=C2A / ATCC 35395 / DSM 2834;	
RX	MEDLINE=21929760; PubMed=11932238; DOI=10.1101/gr.223902;	
RA	Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,	
RA	FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,	
RA	Allen N., Naylor J., Stange-Thomann N., Dehrellano K., Johnson R.,	
RA	Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,	
RA	Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,	
RA	Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,	
RA	Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,	
RA	Springer T.A., Unayam L.A., White O., White R.H., de Macario E.C.,	
RA	Ferry J.G., Jarrell K.F., Jing H., Macario A.J.B., Paulsen I.T.,	
RA	Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,	
RA	Metcalf W.W., Birren B.;	
RT	"The genome of Methanosarcina acetivorans reveals extensive metabolic	
RT	and physiological diversity."	
RL	Genome Res. 12:532-542(2002).	
DR	EMBL; AB010705; AA003895.1; -.	
DR	HSSP; PI4930; IL1D.	
DR	Pfam; PF01641; SelR; 1.	
DR	ProDom; PD004057; DUF25; 1.	
DR	TIGRFAMs; TIGR00357; DUF25; 1.	
KW	Complete proteome.	
SQ	SEQUENCE 147 AA; 16825 MW; B9A891D989BD5943 CRC64;	
Query Match 40.5%; Score 420; DB 2; Length 147;		
Best Local Similarity 52.6%; Pred. No. 9.2e-32;		
Matches 71; Conservative 26; Mismatches 38; Indels 0; Gaps 0;		
QY	42 KVFVSQQLRKRLTPQYHVHTQKGTSAFEGEYTHHKDPGIYKVCVCGTPLFKSETKPD 101	
DB	12 KTEKSEEWKILTPQYHVLRKGTGKPFSGNLVYKKEGVVTCACQQLFSSDTKPE 71	
QY	102 SSGSWPSFDHVINSEAITFTDPSYGMHVRVETSCQCAHLGHIPDDGPRPTGKYCYNS 161	
DB	72 SGTGWPSFYDAISDDKVLKEDNSYFMHRIEYVVCSCGSHLGHVFDGVPVPTGKYCYNS 131	
QY	162 AALSFTPADSSCTAE 176	
DB	132 VSLGFEKEBEAREEE 146	
RESULT 9		
MSRB_SYNEL STANDARD; PRT; 135 AA.		
ID	Q8DJK9;	
AC	Q8DJK9;	
DT	10-OCT-2003 (Rel. 42, Created)	
DT	10-OCT-2003 (Rel. 42, Last sequence update)	
DT	25-OCT-2004 (Rel. 45, Last annotation update)	
DE	Peptide methionine sulfoxide reductase msrB (EC 1.8.4.6).	
GN	Name=msrB; OrderedLocusNames=tl1214;	
OS	Synechococcus elongatus (Thermosynechococcus elongatus).	
OC	Bacteria; Cyanobacteria; Chroococcales; Synechococcus.	
OX	NCBI_TaxID=32046;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=BP-1;	
RX	MEDLINE=2225144; PubMed=12240834;	
RA	Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,	
RA	Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,	
RA	Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,	
RA	Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;	
"Complete genome structure of the thermophilic cyanobacterium		
Thermosynechococcus elongatus BP-1.";		
DNA Res. 9:123-130(2002).		
CC	-1- CATALYTIC ACTIVITY: Protein L-methionine + thioredoxin disulfide =	
CC	protein L-methionine S-oxide + thioredoxin.	
CC	-1- SIMILARITY: Belongs to the msrB Met sulfoxide reductase family.	
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or send an email to license@isb-sib.ch).		
EMBL; AP005373; BAC08766.1; -.		
HSSP; PI4930; IL1D.		
HAWAP; MF_01400; -; 1.		
DR	InterPro; IPR002579; DUF25.	
DR	InterPro; IPR011057; Msa4_like.	
DR	Pfam; PF01641; SelR; 1.	
DR	ProDom; PD004057; DUF25; 1.	
DR	TIGRFAMs; TIGR00357; DUF25; 1.	
KW	Complete proteome; Oxidoreductase.	
FT	ACT SITE 119 119 By similarity.	
SQ	SEQUENCE 135 AA; 15087 MW; 68CBA46572BAAE59 CRC64;	
Query Match 40.3%; Score 417; DB 1; Length 135;		
Best Local Similarity 56.4%; Pred. No. 1.6e-31;		
Matches 75; Conservative 22; Mismatches 36; Indels 0; Gaps 0;		
QY	42 KVFVSQQLRKRLTPQYHVHTQKGTSAFEGEYTHHKDPGIYKVCVCGTPLFKSETKPD 101	
DB	3 KVKYTDAEWQALTPQYVYVTKKGTAFATGTYWNNKPGLYSCVCGTPLFRSETKYD 62	
QY	102 SSGSWPSFDHVINSEAITFTDPSYGMHVRVETSCQCAHLGHIPDDGPRPTGKYCYNS 161	
DB	63 SGTGWPSFWQPLDPNNIRMERDLHSGMVRTEVLCVACDAHLGHVFDGPPPTGLRYCINS 122	
QY	162 AALSFTPADSSGT 174	
DB	123 AALAFVPESAASS 135	
RESULT 10		
Q8PWF5 PRELIMINARY; PRT; 140 AA.		
ID	Q8PWF5;	
AC	Q8PWF5;	
DT	01-OCT-2002 (TrEMBLrel. 22, Created)	
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)	
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)	
DE	Transcriptional regulator.	
GN	OrderedLocusNames=MM1634;	
OS	Methanosarcina mazei (Methanosarcina frisia).	
OC	Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;	
OC	Methanosarcinaceae; Methanosarcina.	
OX	NCBI_TaxID=2209;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=Goe1 / Goe1 / ATCC BAA-199 / DSM 3647 / OCM 88;	
RX	MEDLINE=22120827; PubMed=12125824;	
RA	Deppenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,	
RA	Martinez-Arias R., Henne A., Wierzer A., Baeumer S., Jacobi C.,	
RA	Bruggemann H., Lienard T., Christmann A., Boencke M., Steckel S.,	
RA	Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,	
RA	Fritz H.-J., Gottschalk G.;	
RT	"The genome of Methanosarcina mazei: evidence for lateral gene	
RT	transfer between Bacteria and Archaea."	
RL	J. Mol. Microbiol. Biotechnol. 4:453-461(2002).	
DR	EMBL; AE013397; AM31330.1; -.	
DR	HSSP; PI4930; IL1D.	
DR	InterPro; IPR002579; MsrB.	
DR	InterPro; IPR011057; Msa4_like.	

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OM protein - protein search, using sw model

Run on: September 3, 2005, 02:18:01 ; Search time 22 Seconds
(without alignments)
651.483 Million cell updates/sec

Perfect score: 1036

Sequence: 1 MSPRRTLPRPLSLCLSLCLC.....GTAEGGGCVASPAQDAKEL 192

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 1500 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A-COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B-COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/5A-COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/5B-COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS-COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	410.5	39.6	180	4	US-09-270-767-44790 Sequence 44790, A
2	410.5	39.6	195	4	US-09-270-767-41877 Sequence 41877, A
3	409.5	39.5	164	4	US-09-543-681A-8198 Sequence 8198, Ap
4	406.5	39.2	155	4	US-09-489-039A-7828 Sequence 7828, Ap
5	406.5	39.2	186	4	US-09-252-991A-26314 Sequence 26314, A
6	348.5	33.6	133	4	US-09-640-211A-735 Sequence 735, App
7	348	33.6	143	4	US-09-328-352-6906 Sequence 6906, Ap
8	332	32.0	357	4	US-09-902-540-11587 Sequence 11587, A
9	321.5	31.0	138	4	US-09-540-236-2621 Sequence 2621, Ap
10	303.5	29.3	154	3	US-09-134-001C-3135 Sequence 3135, Ap
11	302.5	29.2	331	4	US-08-961-083-212 Sequence 212, App
12	302.5	29.2	331	4	US-09-536-784-212 Sequence 192, App
13	302.5	29.2	344	3	US-08-961-083-192 Sequence 192, App
14	302.5	29.2	370	4	US-09-583-110-5251 Sequence 5251, Ap
15	302.5	29.2	375	4	US-09-107-433-4121 Sequence 4121, Ap
16	302.5	29.2	375	4	US-08-915-003-7 Sequence 7, Appli
17	292	28.2	521	2	US-08-642-247-7 Sequence 2092, Ap
18	292	28.2	521	2	US-08-642-247-7 Sequence 2092, Ap
19	287.5	27.8	579	4	US-09-540-236-2092 Sequence 3567, Ap
20	285.5	27.6	255	4	US-09-583-110-3567 Sequence 4335, Ap
21	285.5	27.6	257	4	US-09-107-433-4335 Sequence 2, Appli
22	285.5	27.6	312	1	US-08-915-003-2 Sequence 2, Appli
23	285.5	27.6	312	2	US-08-642-247-2 Sequence 19623, A
24	259.5	25.0	144	4	US-09-248-796A-19623 Sequence 5425, Ap
25	171	16.5	115	4	US-09-134-000C-5425 Sequence 10998, A
26	169.5	16.4	140	4	US-09-949-016-10998 Sequence 14, Appli
27	163	15.7	83	3	US-08-665-259-14 Sequence 14, Appli
28	163	15.7	83	3	US-08-762-500-14 Sequence 14, Appli

29	153	14.8	173	2	US-08-245-511-6	Sequence 6, Appli
30	153	14.8	173	2	US-08-245-511-25	Sequence 25, Appli
31	153	14.8	173	2	US-08-600-993A-6	Sequence 6, Appli
32	153	14.8	173	2	US-08-600-993A-25	Sequence 25, Appli
33	144.5	13.9	175	2	US-08-245-511-26	Sequence 26, Appli
34	144.5	13.9	175	2	US-08-600-993A-26	Sequence 26, Appli
35	138	13.3	51	4	US-09-902-540-15273	Sequence 15273, A
36	131	12.6	48	4	US-09-270-767-43822	Sequence 43822, A
37	84.5	8.2	654	4	US-09-270-767-41452	Sequence 41452, A
38	82.5	8.0	61	4	US-09-621-976-7496	Sequence 7496, Ap
39	82	7.9	411	4	US-09-325-256-23	Sequence 23, Appli
40	82	7.9	411	4	US-09-704-917-16	Sequence 16, Appli
41	82	7.9	411	4	US-09-151-999-16	Sequence 16, Appli
42	82	7.9	411	4	US-09-418-221-16	Sequence 16, Appli
43	78	7.5	135	4	US-09-270-767-39872	Sequence 39872, A
44	78	7.5	135	4	US-09-270-767-55089	Sequence 55089, A
45	77	7.4	364	4	US-09-270-767-42122	Sequence 42122, A
46	76.5	7.4	324	4	US-09-270-767-46646	Sequence 46646, A
47	76	7.3	1184	3	US-09-541-782-2	Sequence 2, Appli
48	76	7.3	1184	4	US-09-723-820-2	Sequence 2, Appli
49	76	7.3	1184	4	US-10-270-085-2	Sequence 7029, Ap
50	74.5	7.2	840	4	US-09-949-016-7029	Sequence 2, Appli
51	74.5	7.2	1065	3	US-09-412-545-2	Sequence 2, Appli
52	74.5	7.2	1065	4	US-09-949-016-6541	Sequence 6541, Ap
53	74	7.1	951	4	US-09-248-796A-20520	Sequence 20520, A
54	74	7.1	3224	3	US-08-705-660-34	Sequence 34, Appli
55	74	7.1	3224	3	US-08-989-045-34	Sequence 34, Appli
56	74	7.1	3224	4	US-09-538-092-1161	Sequence 1161, Ap
57	74	7.1	3224	4	US-09-315-355A-34	Sequence 34, Appli
58	73.5	7.1	223	4	US-09-462-246-2	Sequence 2, Appli
59	73	7.0	193	2	US-08-739-485-7	Sequence 7, Appli
60	73	7.0	211	4	US-09-949-016-11606	Sequence 11606, A
61	73	7.0	449	3	US-09-293-505-29	Sequence 29, Appli
62	73	7.0	449	4	US-09-060-939A-29	Sequence 29, Appli
63	73	7.0	1244	4	US-09-538-092-12	Sequence 12, Appli
64	72.5	7.0	977	4	US-09-248-796A-15579	Sequence 15579, A
65	72.5	7.0	1476	4	US-09-817-514A-4	Sequence 4, Appli
66	72	6.9	302	4	US-09-270-767-32413	Sequence 32413, A
67	72	6.9	302	4	US-09-270-767-47630	Sequence 47630, A
68	72	6.9	411	3	US-08-460-900C-10	Sequence 10, Appli
69	72	6.9	411	3	US-08-954-698-10	Sequence 10, Appli
70	72	6.9	411	3	US-08-957-874-10	Sequence 10, Appli
71	72	6.9	411	4	US-09-325-256-19	Sequence 19, Appli
72	72	6.9	411	4	US-09-639-695-10	Sequence 10, Appli
73	72	6.9	411	4	US-09-448-188-10	Sequence 10, Appli
74	72	6.9	411	4	US-08-954-128-10	Sequence 10, Appli
75	72	6.9	411	4	US-09-704-917-12	Sequence 12, Appli
76	72	6.9	411	4	US-08-954-740-10	Sequence 10, Appli
77	72	6.9	411	4	US-09-151-999-12	Sequence 12, Appli
78	72	6.9	411	4	US-09-736-476-10	Sequence 10, Appli
79	72	6.9	411	4	US-09-418-221-12	Sequence 12, Appli
80	72	6.9	636	4	US-09-949-016-11656	Sequence 11656, A
81	72	6.9	638	4	US-09-248-796A-18466	Sequence 18466, A
82	72	6.9	728	4	US-09-949-016-8296	Sequence 8296, Ap
83	71.5	6.9	540	4	US-09-949-016-6358	Sequence 6358, Ap
84	71.5	6.9	564	4	US-09-949-016-11234	Sequence 11234, A
85	71.5	6.9	575	4	US-09-949-016-11265	Sequence 11265, A
86	71.5	6.9	575	4	US-09-949-016-11265	Sequence 11265, A
87	71.5	6.9	575	4	US-09-949-016-11267	Sequence 11267, A
88	71.5	6.9	657	4	US-09-949-016-11365	Sequence 11365, A
89	71.5	6.9	657	4	US-09-949-016-11366	Sequence 11366, A
90	71.5	6.9	657	4	US-09-949-016-11367	Sequence 11367, A
91	71.5	6.9	657	4	US-09-949-016-11368	Sequence 11368, A
92	71.5	6.9	657	4	US-09-949-016-11369	Sequence 11369, A
93	71.5	6.9	677	4	US-09-949-016-11370	Sequence 11370, A
94	71.5	6.9	677	4	US-09-949-016-11370	Sequence 11370, A
95	71.5	6.9	677	4	US-09-949-016-11371	Sequence 11371, A
96	71.5	6.9	677	4	US-09-949-016-11372	Sequence 11372, A
97	71	6.9	139	4	US-09-472-087-25	Sequence 25, Appli
98	71	6.9	139	4	US-09-472-087-114	Sequence 114, Appli
99	71	6.9	370	4	US-09-949-016-8630	Sequence 8630, Ap
100	71	6.9	524	4	US-09-949-016-5897	Sequence 5897, Ap
101	71	6.9	541	4	US-09-949-016-9092	Sequence 9092, Ap

102	70.5	6.8	1481	3	US-09-251-645-14	Sequence 14, Appl	175	69	6.7	788	4	US-09-949-016-5901	Sequence 5901, Ap
103	70.5	6.8	1742	4	US-09-386-962C-4	Sequence 4, Appl	176	68.5	6.6	138	4	US-09-134-000C-5490	Sequence 5490, Ap
104	70.5	6.8	1742	4	US-09-386-959-4	Sequence 4, Appl	177	68.5	6.6	338	2	US-08-933-750C-4	Sequence 4, Appl
105	70	6.8	155	4	US-09-513-999C-5965	Sequence 5965, Ap	178	68.5	6.6	338	3	US-09-234-613-4	Sequence 8, Appl
106	70	6.8	168	4	US-09-621-976-5050	Sequence 5050, Ap	179	68	6.6	194	2	US-08-739-485-8	Sequence 8, Appl
107	70	6.8	193	1	US-08-616-368A-9	Sequence 9, Appl	180	68	6.6	291	4	US-09-270-767-33233	Sequence 33233, A
108	70	6.8	193	3	US-09-054-298-9	Sequence 9, Appl	181	68	6.6	557	4	US-09-949-016-6279	Sequence 6279, Ap
109	70	6.8	193	3	US-08-818-655-9	Sequence 9, Appl	182	68	6.6	564	4	US-09-949-016-9503	Sequence 9503, Ap
110	70	6.8	193	4	US-09-305-839-9	Sequence 9, Appl	183	68	6.6	591	2	US-08-889-402-1	Sequence 1, Appl
111	70	6.8	198	4	US-09-270-767-37065	Sequence 37065, A	184	68	6.6	605	2	US-08-889-402-2	Sequence 2, Appl
112	70	6.8	198	4	US-09-270-767-52282	Sequence 52282, A	185	68	6.6	671	3	US-09-196-390-2	Sequence 2, Appl
113	70	6.8	556	4	US-09-252-991A-27601	Sequence 27601, A	186	68	6.6	671	4	US-09-952-677-2	Sequence 2, Appl
114	70	6.8	2476	4	US-09-824-574-7	Sequence 7, Appl	187	68	6.6	737	4	US-09-949-016-9829	Sequence 9829, Ap
115	69.5	6.7	310	1	US-08-078-683A-3	Sequence 3, Appl	188	68	6.6	1050	4	US-09-902-540-16666	Sequence 16666, A
116	69.5	6.7	310	2	US-08-488-199-4	Sequence 4, Appl	189	67.5	6.5	184	4	US-09-248-796A-15913	Sequence 15913, A
117	69.5	6.7	310	4	US-08-471-970A-3	Sequence 3, Appl	190	67.5	6.5	340	4	US-09-949-016-10568	Sequence 10568, A
118	69.5	6.7	310	4	US-09-723-677B-3	Sequence 3, Appl	191	67.5	6.5	445	3	US-08-592-900-2	Sequence 2, Appl
119	69.5	6.7	310	4	US-09-949-016-6296	Sequence 6296, Ap	192	67.5	6.5	445	3	US-09-252-292C-28	Sequence 28, Appl
120	69.5	6.7	351	4	US-09-118-426-6	Sequence 6, Appl	193	67.5	6.5	445	4	US-09-567-615B-9	Sequence 9, Appl
121	69.5	6.7	359	4	US-09-425-488-2	Sequence 2, Appl	194	67.5	6.5	446	3	US-08-979-917A-1	Sequence 1, Appl
122	69.5	6.7	362	4	US-09-949-016-9134	Sequence 9134, Ap	195	67.5	6.5	633	4	US-09-581-001B-12	Sequence 12, Appl
123	69.5	6.7	373	4	US-09-118-426-5	Sequence 5, Appl	196	67.5	6.5	647	4	US-09-452-846B-4	Sequence 4, Appl
124	69.5	6.7	374	3	US-08-818-112-153	Sequence 153, App	197	67.5	6.5	2647	2	US-08-583-562B-8	Sequence 8, Appl
125	69.5	6.7	374	3	US-08-818-111-148	Sequence 148, App	198	67.5	6.5	2647	2	US-08-779-113-8	Sequence 8, Appl
126	69.5	6.7	374	3	US-09-056-556-153	Sequence 153, App	199	67.5	6.5	2647	4	US-09-949-016-6082	Sequence 6082, Ap
127	69.5	6.7	374	3	US-09-056-556-155	Sequence 155, App	200	67.5	6.5	2666	4	US-09-949-016-10857	Sequence 10857, A
128	69.5	6.7	374	4	US-09-072-596-148	Sequence 148, App	201	67	6.5	111	3	US-09-091-725-39	Sequence 39, Appl
129	69.5	6.7	374	4	US-09-072-596-150	Sequence 150, App	202	67	6.5	385	4	US-09-252-991A-18126	Sequence 18126, A
130	69.5	6.7	374	4	US-09-072-967-153	Sequence 153, App	203	67	6.5	406	1	US-09-270-767-41627	Sequence 41627, A
131	69.5	6.7	374	4	US-09-072-967-155	Sequence 155, App	204	67	6.5	706	2	US-08-074-967-2	Sequence 2, Appl
132	69.5	6.7	374	4	US-09-287-849-6	Sequence 6, Appl	205	67	6.5	706	2	US-08-553-541B-2	Sequence 2, Appl
133	69.5	6.7	374	4	US-09-287-849-40	Sequence 40, Appl	206	67	6.5	706	3	US-09-268-202-2	Sequence 2, Appl
134	69.5	6.7	414	3	US-09-334-601-4	Sequence 4, Appl	207	67	6.5	706	4	US-09-538-092-1104	Sequence 1104, Ap
135	69.5	6.7	508	4	US-09-902-540-10562	Sequence 10562, A	208	67	6.5	706	5	US-09-761-117-2	Sequence 2, Appl
136	69.5	6.7	652	4	US-09-072-596-350	Sequence 350, App	209	67	6.5	706	5	FCT-US94-06669-2	Sequence 2, Appl
137	69.5	6.7	652	4	US-09-072-967-355	Sequence 355, App	210	67	6.5	757	4	US-09-949-016-7121	Sequence 7121, Ap
138	69.5	6.7	802	3	US-09-056-556-214	Sequence 214, App	211	67	6.5	1121	3	US-09-171-461-28	Sequence 28, Appl
139	69.5	6.7	802	4	US-09-072-596-209	Sequence 209, App	212	67	6.5	1121	5	US-09-970-711-28	Sequence 28, Appl
140	69.5	6.7	802	4	US-09-072-596-346	Sequence 346, App	213	67	6.5	1251	5	FCT-US95-02251-3	Sequence 3, Appl
141	69.5	6.7	802	4	US-09-072-967-214	Sequence 214, App	214	67	6.5	1252	1	US-08-199-780-3	Sequence 3, Appl
142	69.5	6.7	802	4	US-09-072-967-351	Sequence 351, App	215	67	6.5	1252	1	US-08-316-650-3	Sequence 3, Appl
143	69.5	6.7	802	4	US-09-287-849-10	Sequence 10, Appl	216	67	6.5	1253	3	US-08-479-722B-4	Sequence 4, Appl
144	69.5	6.7	1670	4	US-09-949-016-5883	Sequence 5883, Ap	217	67	6.5	1253	4	US-09-592-685-4	Sequence 4, Appl
145	69	6.7	193	1	US-08-616-368A-1	Sequence 1, Appl	218	67	6.5	2409	6	5180808-2	Patent No. 5180808
146	69	6.7	193	1	US-08-616-368A-8	Sequence 8, Appl	219	67	6.5	2409	6	5180808-2	Patent No. 5180808
147	69	6.7	193	1	US-08-616-368A-13	Sequence 13, Appl	220	66.5	6.4	258	3	US-08-303-861-18	Sequence 18, Appl
148	69	6.7	193	2	US-08-739-485-9	Sequence 9, Appl	221	66.5	6.4	258	3	US-08-303-861-19	Sequence 19, Appl
149	69	6.7	193	3	US-09-054-298-1	Sequence 1, Appl	222	66.5	6.4	258	3	US-09-213-343-2	Sequence 2, Appl
150	69	6.7	193	3	US-09-054-298-8	Sequence 8, Appl	223	66.5	6.4	291	4	US-09-902-540-14575	Sequence 14575, A
151	69	6.7	193	3	US-09-054-298-13	Sequence 13, Appl	224	66.5	6.4	306	4	US-09-101-368-10	Sequence 10, Appl
152	69	6.7	193	3	US-08-818-655-1	Sequence 1, Appl	225	66.5	6.4	437	3	US-08-757-230A-2	Sequence 2, Appl
153	69	6.7	193	3	US-08-818-655-8	Sequence 8, Appl	226	66.5	6.4	437	3	US-08-757-230A-9	Sequence 9, Appl
154	69	6.7	193	3	US-08-818-655-13	Sequence 13, Appl	227	66.5	6.4	437	5	US-08-700-393-2	Sequence 2, Appl
155	69	6.7	193	4	US-09-305-839-1	Sequence 1, Appl	228	66.5	6.4	437	5	FCT-US95-02315-2	Sequence 2, Appl
156	69	6.7	193	4	US-09-305-839-8	Sequence 8, Appl	229	66.5	6.4	491	4	US-09-538-092-544	Sequence 544, App
157	69	6.7	193	4	US-09-305-839-13	Sequence 13, Appl	230	66.5	6.4	559	4	US-09-512-260A-3	Sequence 3, Appl
158	69	6.7	219	4	US-09-949-016-9338	Sequence 9338, Ap	231	66.5	6.4	803	3	US-09-063-035-2	Sequence 2, Appl
159	69	6.7	258	4	US-09-270-767-43579	Sequence 43579, A	232	66.5	6.4	1656	4	US-09-489-039A-13773	Sequence 13773, A
160	69	6.7	429	4	US-09-949-016-9689	Sequence 9689, Ap	233	66.5	6.4	1821	4	US-09-949-016-7247	Sequence 7247, Ap
161	69	6.7	543	4	US-09-362-123A-4	Sequence 4, Appl	234	66.5	6.4	1821	1	US-09-949-016-5938	Sequence 5938, Ap
162	69	6.7	718	1	US-08-444-792-4	Sequence 4, Appl	235	66	6.4	194	1	US-08-616-368A-11	Sequence 11, Appl
163	69	6.7	718	1	US-08-445-042-4	Sequence 4, Appl	236	66	6.4	194	3	US-09-054-298-11	Sequence 11, Appl
164	69	6.7	784	4	US-09-949-016-9467	Sequence 9467, Ap	237	66	6.4	194	3	US-08-818-655-11	Sequence 11, Appl
165	69	6.7	784	2	US-07-728-215-32	Sequence 32, Appl	238	66	6.4	194	4	US-09-305-839-11	Sequence 11, Appl
166	69	6.7	788	3	US-08-938-085A-32	Sequence 32, Appl	239	66	6.4	522	4	US-09-270-767-43235	Sequence 43235, A
167	69	6.7	788	3	US-09-409-648-3	Sequence 3, Appl	240	66	6.4	522	4	US-09-585-858-59	Sequence 59, Appl
168	69	6.7	788	3	US-09-409-648-4	Sequence 4, Appl	241	66	6.4	522	4	US-10-270-878-59	Sequence 59, Appl
169	69	6.7	788	3	US-09-409-648-32	Sequence 32, Appl	242	66	6.4	669	3	US-09-342-647-18	Sequence 18, Appl
170	69	6.7	788	4	US-10-072-844-32	Sequence 32, Appl	243	66	6.4	726	4	US-09-949-016-10050	Sequence 10050, A
171	69	6.7	788	4	US-10-072-838-32	Sequence 32, Appl	244	66	6.4	782	4	US-09-270-767-42104	Sequence 42104, A
172	69	6.7	788	4	US-10-072-841A-32	Sequence 32, Appl	245	66	6.4	784	4	US-09-198-452A-288	Sequence 288, App
173	69	6.7	788	4	US-09-054-272-8	Sequence 8, Appl	246	66	6.4	806	4	US-09-438-185A-277	Sequence 277, App
174	69	6.7	788	4	US-09-054-272-44	Sequence 44, Appl	247	66	6.4	871	4	US-09-585-858-36	Sequence 36, Appl

248	66	6.4	871	4	US-10-270-878-36	Sequence 36, Appl	321	64	6.2	485	3	US-08-683-838A-12	Sequence 12, Appl
249	66	6.4	3084	4	US-09-562-702A-12	Sequence 10, Appl	322	64	6.2	485	3	US-08-600-656-1	Sequence 1, Appl
250	66	6.4	3106	4	US-09-562-702A-10	Sequence 10, Appl	323	64	6.2	485	3	US-09-170-670-1	Sequence 1, Appl
251	65.5	6.3	112	4	US-09-840-459-70	Sequence 70, Appl	324	64	6.2	485	3	US-09-170-670-7	Sequence 7, Appl
252	65.5	6.3	112	4	US-09-497-625A-70	Sequence 70, Appl	325	64	6.2	485	3	US-09-193-068-1	Sequence 7, Appl
253	65.5	6.3	163	4	US-09-270-767-32837	Sequence 32837, A	326	64	6.2	485	3	US-09-133-068-7	Sequence 7, Appl
254	65.5	6.3	234	4	US-09-338-920B-11	Sequence 11, Appl	327	64	6.2	485	3	US-09-183-412-1	Sequence 7, Appl
255	65.5	6.3	271	4	US-09-248-796A-20168	Sequence 20168, A	328	64	6.2	485	3	US-09-183-412-7	Sequence 7, Appl
256	65.5	6.3	327	4	US-09-949-016-7575	Sequence 7575, Ap	329	64	6.2	485	3	US-09-264-097-1	Sequence 7, Appl
257	65.5	6.3	423	1	US-08-445-746-2	Sequence 2, Appl	330	64	6.2	485	3	US-09-354-191A-1	Sequence 1, Appl
258	65.5	6.3	423	3	US-09-008-722-2	Sequence 2, Appl	331	64	6.2	485	3	US-09-291-023A-19	Sequence 19, Appl
259	65.5	6.3	712	4	US-09-270-767-46235	Sequence 46235, A	332	64	6.2	485	3	US-09-290-734-1	Sequence 7, Appl
260	65.5	6.3	726	4	US-09-949-016-5916	Sequence 5916, Ap	333	64	6.2	485	3	US-09-290-734-7	Sequence 7, Appl
261	65.5	6.3	737	4	US-09-949-016-11607	Sequence 11607, A	334	64	6.2	485	4	US-09-636-252A-12	Sequence 12, Appl
262	65.5	6.3	1155	4	US-09-710-279-1780	Sequence 1780, Ap	335	64	6.2	485	4	US-09-381-687-2	Sequence 2, Appl
263	65.5	6.3	1935	4	US-09-949-016-10403	Sequence 10403, A	336	64	6.2	485	4	US-09-545-586-1	Sequence 1, Appl
264	65.5	6.3	2471	1	US-08-185-432-16	Sequence 16, Appl	337	64	6.2	485	4	US-09-545-586-7	Sequence 7, Appl
265	65.5	6.3	2471	3	US-08-083-590A-19	Sequence 19, Appl	338	64	6.2	485	4	US-09-540-715A-19	Sequence 19, Appl
266	65.5	6.3	2471	3	US-08-532-384-19	Sequence 19, Appl	339	64	6.2	485	4	US-09-769-864-7	Sequence 7, Appl
267	65.5	6.3	2471	4	US-08-899-232-1	Sequence 1, Appl	340	64	6.2	486	4	US-09-381-687-4	Sequence 4, Appl
268	65.5	6.3	2471	4	US-09-121-457-1	Sequence 1, Appl	341	64	6.2	574	4	US-09-921-099A-7	Sequence 7, Appl
269	65.5	6.3	2871	4	US-09-538-092-1076	Sequence 1076, Ap	342	64	6.2	687	3	US-09-342-647-28	Sequence 28, Appl
270	65	6.3	193	2	US-08-739-485-1	Sequence 1, Appl	343	64	6.2	687	4	US-09-107-433-3382	Sequence 3382, Ap
271	65	6.3	242	4	US-09-602-777A-92	Sequence 92, Appl	344	64	6.2	695	3	US-09-153-277-2	Sequence 2, Appl
272	65	6.3	243	4	US-09-107-532A-4665	Sequence 4665, Ap	345	64	6.2	700	4	US-09-621-816B-2	Sequence 2, Appl
273	65	6.3	246	2	US-08-720-258-2	Sequence 2, Appl	346	64	6.2	700	4	US-09-583-110-4537	Sequence 4537, Ap
274	65	6.3	246	4	US-09-396-840-4	Sequence 4, Appl	347	64	6.2	788	4	US-09-270-767-44611	Sequence 44611, A
275	65	6.3	267	4	US-09-602-777A-90	Sequence 90, Appl	348	64	6.2	788	4	US-09-270-767-38876	Sequence 38876, A
276	65	6.3	430	1	US-08-535-237-2	Sequence 3, Appl	349	63.5	6.1	134	4	US-09-270-767-54093	Sequence 54093, A
277	65	6.3	430	3	US-09-468-265-3	Sequence 3, Appl	350	63.5	6.1	134	4	US-09-270-767-33767	Sequence 33767, A
278	65	6.3	689	4	US-08-778-570B-16	Sequence 16, Appl	351	63.5	6.1	163	4	US-09-286-529-3	Sequence 3, Appl
279	65	6.3	689	4	US-09-059-584-16	Sequence 16, Appl	352	63.5	6.1	210	3	US-09-134-000C-5802	Sequence 5802, Ap
280	65	6.3	709	4	US-08-778-570B-15	Sequence 15, Appl	353	63.5	6.1	254	4	US-09-586-106D-107	Sequence 107, App
281	65	6.3	709	4	US-09-059-584-15	Sequence 15, Appl	354	63.5	6.1	254	4	US-09-198-452A-503	Sequence 503, App
282	65	6.3	803	4	US-09-538-092-1026	Sequence 1026, Ap	355	63.5	6.1	275	4	US-09-438-185A-470	Sequence 470, App
283	65	6.3	1047	4	US-10-144-198-36	Sequence 36, Appl	356	63.5	6.1	437	1	US-08-176-427B-8	Sequence 8, Appl
284	65	6.3	1041	4	US-10-144-198-14	Sequence 14, Appl	357	63.5	6.1	437	2	US-08-356-060A-11	Sequence 11, Appl
285	64.5	6.2	114	4	US-09-513-999C-5016	Sequence 5016, Ap	358	63.5	6.1	437	3	US-08-946-329A-20	Sequence 20, Appl
286	64.5	6.2	154	4	US-09-902-540-13271	Sequence 13271, A	359	63.5	6.1	437	3	US-08-567-357A-20	Sequence 20, Appl
287	64.5	6.2	231	4	US-09-107-532A-3675	Sequence 3675, Ap	360	63.5	6.1	437	3	US-08-460-900C-11	Sequence 11, Appl
288	64.5	6.2	296	4	US-09-107-532A-4943	Sequence 4943, Ap	361	63.5	6.1	437	3	US-08-723-743A-20	Sequence 20, Appl
289	64.5	6.2	472	4	US-09-252-991A-26921	Sequence 26921, A	362	63.5	6.1	437	3	US-08-674-509B-11	Sequence 11, Appl
290	64.5	6.2	564	3	US-09-360-197-16	Sequence 16, Appl	363	63.5	6.1	437	3	US-08-954-698-11	Sequence 11, Appl
291	64.5	6.2	618	4	US-09-248-796A-20967	Sequence 20967, A	364	63.5	6.1	437	3	US-09-057-860A-6	Sequence 6, Appl
292	64.5	6.2	997	4	US-09-747-371-3	Sequence 3, Appl	365	63.5	6.1	437	3	US-08-349-498-20	Sequence 20, Appl
293	64.5	6.2	2161	3	US-09-081-320-3	Sequence 3, Appl	366	63.5	6.1	437	3	US-09-293-505-14	Sequence 14, Appl
294	64.5	6.2	2161	3	US-09-574-141A-3	Sequence 3, Appl	367	63.5	6.1	437	3	US-09-325-256-20	Sequence 20, Appl
295	64.5	6.2	2161	3	US-09-707-780-3	Sequence 3, Appl	368	63.5	6.1	437	3	US-09-448-188-11	Sequence 11, Appl
296	64.5	6.2	2161	4	US-09-568-189A-3	Sequence 3, Appl	369	63.5	6.1	437	4	US-09-639-695-11	Sequence 11, Appl
297	64.5	6.2	3418	2	US-08-639-501-2	Sequence 2, Appl	370	63.5	6.1	437	4	US-09-448-188-11	Sequence 11, Appl
298	64.5	6.2	3418	2	US-08-603-753D-4	Sequence 4, Appl	371	63.5	6.1	437	4	US-09-954-128-11	Sequence 11, Appl
299	64.5	6.2	3418	3	US-09-044-946-2	Sequence 2, Appl	372	63.5	6.1	437	4	US-09-704-917-13	Sequence 13, Appl
300	64.5	6.2	3418	3	US-08-755-587-44	Sequence 44, Appl	373	63.5	6.1	437	4	US-08-954-740-11	Sequence 11, Appl
301	64.5	6.2	3418	3	US-09-044-908-2	Sequence 2, Appl	374	63.5	6.1	437	4	PCT-US95-15463-20	Sequence 20, Appl
302	64.5	6.2	3418	3	US-09-099-753-4	Sequence 4, Appl	375	63.5	6.1	437	5	PCT-US95-15923-20	Sequence 20, Appl
303	64.5	6.2	3418	3	US-08-986-106-4	Sequence 4, Appl	376	63.5	6.1	462	1	US-08-748-591-4	Sequence 4, Appl
304	64	6.2	86	3	US-08-654-737B-2	Sequence 2, Appl	377	63.5	6.1	462	1	US-08-748-591-9	Sequence 9, Appl
305	64	6.2	220	4	US-09-270-767-43986	Sequence 43986, A	378	63.5	6.1	475	2	US-08-356-060A-13	Sequence 13, Appl
306	64	6.2	240	1	US-08-488-113B-147	Sequence 147, App	379	63.5	6.1	475	2	US-08-460-900C-13	Sequence 13, Appl
307	64	6.2	240	1	US-08-477-484B-147	Sequence 147, App	380	63.5	6.1	475	3	US-08-674-509B-13	Sequence 13, Appl
308	64	6.2	240	2	US-08-646-360-147	Sequence 147, App	381	63.5	6.1	475	3	US-08-954-698-13	Sequence 13, Appl
309	64	6.2	240	3	US-08-839-765-147	Sequence 147, App	382	63.5	6.1	475	3	US-08-954-698-13	Sequence 13, Appl
310	64	6.2	240	3	US-09-136-389-147	Sequence 147, App	383	63.5	6.1	475	4	US-09-325-256-22	Sequence 22, Appl
311	64	6.2	240	3	US-09-610-838-147	Sequence 147, App	384	63.5	6.1	475	4	US-09-639-695-13	Sequence 13, Appl
312	64	6.2	240	4	US-09-711-485-147	Sequence 147, App	385	63.5	6.1	475	4	US-09-448-188-13	Sequence 13, Appl
313	64	6.2	262	2	US-08-038-761A-1	Sequence 1, Appl	386	63.5	6.1	475	4	US-08-954-128-13	Sequence 13, Appl
314	64	6.2	325	4	US-09-599-360B-74	Sequence 74, Appl	387	63.5	6.1	475	4	US-09-325-256-22	Sequence 22, Appl
315	64	6.2	354	4	US-09-252-991A-20132	Sequence 20132, A	388	63.5	6.1	475	4	US-09-639-695-13	Sequence 13, Appl
316	64	6.2	420	4	US-09-248-796A-20491	Sequence 20491, A	389	63.5	6.1	475	4	US-09-448-188-13	Sequence 13, Appl
317	64	6.2	425	4	US-09-748-537-14	Sequence 14, Appl	390	63.5	6.1	475	4	US-08-954-128-13	Sequence 13, Appl
318	64	6.2	485	2	US-08-446-803-1	Sequence 1, Appl	391	63.5	6.1	475	4	US-09-704-917-15	Sequence 15, Appl
319	64	6.2	485	2	US-08-861-837-1	Sequence 1, Appl	392	63.5	6.1	475	4		
320	64	6.2	485	2	US-08-600-908A-12	Sequence 12, Appl	393	63.5	6.1	475	4		

394	63.5	6.1	475	4	US-08-954-740-13	Sequence 13, Appl	467	63	6.1	1079	3	US-08-484-719B-8	Sequence 8, Appl
395	63.5	6.1	475	4	US-09-151-999-15	Sequence 15, Appl	468	63	6.1	1079	3	US-08-484-159-8	Sequence 8, Appl
396	63.5	6.1	475	4	US-09-736-476-13	Sequence 13, Appl	469	63	6.1	1091	1	US-07-595-564-3	Sequence 3, Appl
397	63.5	6.1	475	4	US-09-021-660A-39	Sequence 39, Appl	470	63	6.1	1091	1	US-08-241-387-3	Sequence 3, Appl
398	63.5	6.1	475	4	US-09-418-221-15	Sequence 15, Appl	471	62.5	6.0	134	3	US-08-981-739-81	Sequence 81, Appl
399	63.5	6.1	484	4	US-09-878-281A-198	Sequence 198, App	472	62.5	6.0	134	4	US-09-128-026-81	Sequence 81, Appl
400	63.5	6.1	577	4	US-09-489-039A-8770	Sequence 8770, Ap	473	62.5	6.0	134	4	US-09-220-616-81	Sequence 81, Appl
401	63.5	6.1	599	3	US-09-352-990-10	Sequence 10, Appl	474	62.5	6.0	134	4	US-09-220-527-81	Sequence 111, App
402	63.5	6.1	711	2	US-08-820-170A-10	Sequence 10, Appl	475	62.5	6.0	142	3	US-08-931-858B-111	Sequence 111, App
403	63.5	6.1	711	3	US-09-055-699-10	Sequence 10, Appl	476	62.5	6.0	142	3	US-08-981-739-111	Sequence 111, App
404	63.5	6.1	711	3	US-09-273-565-10	Sequence 10, Appl	477	62.5	6.0	142	4	US-09-128-026-111	Sequence 111, App
405	63.5	6.1	711	3	US-09-565-538-10	Sequence 10, Appl	478	62.5	6.0	142	4	US-09-220-616-111	Sequence 111, App
406	63.5	6.1	711	3	US-09-661-468-10	Sequence 10, Appl	479	62.5	6.0	142	4	US-09-220-527-111	Sequence 111, App
407	63.5	6.1	711	4	US-09-976-165-10	Sequence 10, Appl	480	62.5	6.0	142	4	US-09-220-407-111	Sequence 111, App
408	63.5	6.1	711	4	US-09-828-648-2	Sequence 2, Appl	481	62.5	6.0	165	4	US-09-270-767-45134	Sequence 45134, A
409	63.5	6.1	740	4	US-09-489-039A-13001	Sequence 13001, A	482	62.5	6.0	185	3	US-08-981-739-133	Sequence 133, App
410	63.5	6.1	765	4	US-09-949-016-10117	Sequence 10117, A	483	62.5	6.0	185	4	US-09-128-026-133	Sequence 133, App
411	63.5	6.1	1503	3	US-08-976-255-14	Sequence 14, Appl	484	62.5	6.0	185	4	US-09-220-616-133	Sequence 133, App
412	63	6.1	179	4	US-09-148-545-177	Sequence 177, App	485	62.5	6.0	185	4	US-09-220-527-133	Sequence 133, App
413	63	6.1	199	4	US-09-248-796A-27769	Sequence 27769, A	486	62.5	6.0	185	4	US-09-248-796A-27611	Sequence 27611, A
414	63	6.1	247	4	US-09-107-532A-5422	Sequence 5422, Ap	487	62.5	6.0	187	4	US-09-248-796A-18921	Sequence 18921, A
415	63	6.1	318	1	US-08-537-942A-1	Sequence 1, Appl	488	62.5	6.0	256	4	US-09-485-529-5	Sequence 5, Appl
416	63	6.1	318	3	US-08-997-252A-1	Sequence 1, Appl	489	62.5	6.0	262	4	US-09-248-796A-17243	Sequence 17243, A
417	63	6.1	318	3	US-09-517-739-1	Sequence 1, Appl	490	62.5	6.0	298	3	US-09-318-661-2	Sequence 2, Appl
418	63	6.1	318	4	US-09-935-720A-1	Sequence 1, Appl	491	62.5	6.0	298	4	US-09-893-758-2	Sequence 2, Appl
419	63	6.1	323	4	US-09-270-767-61011	Sequence 61011, A	492	62.5	6.0	317	3	US-09-141-027-3	Sequence 3, Appl
420	63	6.1	336	4	US-09-949-016-10050	Sequence 10050, A	493	62.5	6.0	317	4	US-09-617-804-3	Sequence 3, Appl
421	63	6.1	340	4	US-09-564-357-3	Sequence 3, Appl	494	62.5	6.0	370	4	US-09-377-285B-16	Sequence 16, Appl
422	63	6.1	343	3	US-09-949-016-11301	Sequence 11301, A	495	62.5	6.0	442	4	US-09-828-062-7	Sequence 7, Appl
423	63	6.1	353	3	US-09-013-881-3	Sequence 3, Appl	496	62.5	6.0	444	4	US-09-252-991A-20775	Sequence 20775, A
424	63	6.1	353	4	US-09-612-473-3	Sequence 3, Appl	497	62.5	6.0	457	4	US-09-389-956-68	Sequence 68, Appl
425	63	6.1	365	2	US-08-846-762-80	Sequence 80, Appl	498	62.5	6.0	533	4	US-09-388-743-10	Sequence 10, Appl
426	63	6.1	365	2	US-08-576-626A-46	Sequence 46, Appl	499	62.5	6.0	533	4	US-10-044-543-10	Sequence 20, Appl
427	63	6.1	381	1	US-07-772-087-6	Sequence 6, Appl	500	62.5	6.0	581	4	US-09-244-805-27	Sequence 27, Appl
428	63	6.1	381	1	US-08-173-508-12	Sequence 12, Appl	501	62.5	6.0	615	4	US-09-345-473E-49	Sequence 49, Appl
429	63	6.1	381	2	US-08-265-310-12	Sequence 12, Appl	502	62.5	6.0	647	4	US-09-389-956-6	Sequence 6, Appl
430	63	6.1	381	3	US-08-951-742-12	Sequence 12, Appl	503	62.5	6.0	705	3	US-09-134-001C-5356	Sequence 5356, Ap
431	63	6.1	382	1	US-08-460-343B-2	Sequence 2, Appl	504	62.5	6.0	917	4	US-08-259-451-11	Sequence 11, Appl
432	63	6.1	382	1	US-08-398-028B-2	Sequence 2, Appl	505	62.5	6.0	1414	4	US-09-438-185A-446	Sequence 446, App
433	63	6.1	382	2	US-08-504-265B-75	Sequence 2, Appl	506	62.5	6.0	1481	2	US-08-616-844-40	Sequence 40, Appl
434	63	6.1	382	2	US-08-504-265B-75	Sequence 75, Appl	507	62.5	6.0	1481	2	US-08-599-654-40	Sequence 40, Appl
435	63	6.1	382	3	US-09-255-502-2	Sequence 2, Appl	508	62.5	6.0	1481	3	US-08-944-868A-40	Sequence 40, Appl
436	63	6.1	382	3	US-09-178-155-2	Sequence 2, Appl	509	62.5	6.0	1481	3	US-08-944-423A-40	Sequence 40, Appl
437	63	6.1	382	3	US-09-445-472-31	Sequence 31, Appl	510	62.5	6.0	1481	3	US-08-944-496-40	Sequence 40, Appl
438	63	6.1	382	4	US-09-178-173A-2	Sequence 2, Appl	511	62.5	6.0	2636	4	US-09-252-991A-25753	Sequence 25753, A
439	63	6.1	382	4	US-09-659-749-2	Sequence 2, Appl	512	62	6.0	161	4	US-09-248-796A-17503	Sequence 17503, A
440	63	6.1	382	4	US-09-672-105-2	Sequence 2, Appl	513	62	6.0	216	4	US-09-311-021-24	Sequence 24, Appl
441	63	6.1	382	4	US-09-177-353-2	Sequence 2, Appl	514	62	6.0	223	4	US-09-248-796A-17647	Sequence 17647, A
442	63	6.1	382	4	US-10-090-624-31	Sequence 31, Appl	515	62	6.0	234	4	US-09-198-452A-608	Sequence 608, App
443	63	6.1	382	4	US-10-033-325-2	Sequence 2, Appl	516	62	6.0	234	4	US-09-438-185A-571	Sequence 571, App
444	63	6.1	382	4	US-09-529-904-2	Sequence 2, Appl	517	62	6.0	245	4	US-09-533-029-44	Sequence 44, Appl
445	63	6.1	382	6	5472855-2	Patent No. 5472855	518	62	6.0	272	4	US-09-252-991A-29681	Sequence 29681, A
446	63	6.1	382	6	5472855-2	Patent No. 5472855	519	62	6.0	277	5	US-09-513-999C-7813	Sequence 7813, Ap
447	63	6.1	410	3	US-08-725-758A-4	Sequence 4, Appl	520	62	6.0	277	5	PCT-US96-05611A-22	Sequence 22, Appl
448	63	6.1	410	4	US-09-735-251-4	Sequence 4, Appl	521	62	6.0	287	3	US-08-985-950-6	Sequence 6, Appl
449	63	6.1	426	3	US-08-725-758A-2	Sequence 2, Appl	522	62	6.0	287	3	US-08-985-950-8	Sequence 8, Appl
450	63	6.1	426	4	US-09-735-251-2	Sequence 2, Appl	523	62	6.0	287	4	US-09-546-049-6	Sequence 6, Appl
451	63	6.1	431	4	US-09-270-767-45503	Sequence 45503, A	524	62	6.0	287	4	US-09-546-049-8	Sequence 8, Appl
452	63	6.1	439	4	US-09-252-991A-25149	Sequence 25149, A	525	62	6.0	423	4	US-09-485-473-1	Sequence 1, Appl
453	63	6.1	518	4	US-09-881-578A-4	Sequence 4, Appl	526	62	6.0	534	3	US-08-755-587-14	Sequence 14, Appl
454	63	6.1	524	4	US-09-242-913B-15	Sequence 15, Appl	527	62	6.0	619	1	US-08-472-934-4	Sequence 4, Appl
455	63	6.1	533	4	US-09-902-540-11053	Sequence 11053, A	528	62	6.0	619	2	US-08-323-460A-4	Sequence 4, Appl
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457	63	6.1	700	2	US-07-862-588B-2	Sequence 2, Appl	530	62	6.0	619	2	US-08-461-146C-12	Sequence 12, Appl
458	63	6.1	737	4	US-09-772-647-4	Sequence 4, Appl	531	62	6.0	619	3	US-08-461-145C-4	Sequence 4, Appl
459	63	6.1	825	4	US-09-270-767-45321	Sequence 45321, A	532	62	6.0	619	3	US-08-461-145C-12	Sequence 12, Appl
460	63	6.1	1073	1	US-07-695-564-1	Sequence 1, Appl	533	62	6.0	619	3	US-09-423-890-10	Sequence 10, Appl
461	63	6.1	1073	1	US-08-241-387-1	Sequence 1, Appl	534	62	6.0	619	3	US-08-628-829-6	Sequence 6, Appl
462	63	6.1	1079	1	US-08-485-588-8	Sequence 8, Appl	535	62	6.0	619	3	US-08-628-829-8	Sequence 8, Appl
463	63	6.1	1079	2	US-08-484-565-8	Sequence 8, Appl	536	62	6.0	739	4	US-09-949-016-7559	Sequence 7559, Ap
464	63	6.1	1079	2	US-08-480-751-8	Sequence 8, Appl	537	62	6.0	770	4	US-09-489-039A-7872	Sequence 7872, Ap
465	63	6.1	1079	2	US-08-943-986-8	Sequence 8, Appl	538	62	6.0	873	3	US-09-187-331-6	Sequence 6, Appl
466	63	6.1	1079	3	US-08-353-784-8	Sequence 8, Appl	539	62	6.0				

540	62	6.0	873	3	US-09-470-946-6	Sequence 6, Appli	613	5.9	327	4	US-09-270-767-57436	Sequence 57436, A
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543	62	6.0	911	2	US-08-478-435-95	Sequence 95, Appli	615	5.9	327	4	US-08-270-767-60376	Sequence 60376, A
544	62	6.0	911	2	US-08-337-483-95	Sequence 95, Appli	616	5.9	327	4	US-08-270-767-60376	Sequence 60376, A
545	62	6.0	911	2	US-08-478-373-95	Sequence 95, Appli	617	5.9	335	4	US-09-270-767-42334	Sequence 42334, A
546	62	6.0	911	2	US-08-478-373-95	Sequence 95, Appli	618	5.9	341	4	US-09-270-767-46584	Sequence 46584, A
547	62	6.0	911	3	US-08-474-671-95	Sequence 95, Appli	619	5.9	379	4	US-09-328-352-5405	Sequence 5405, Ap
548	62	6.0	911	3	US-08-483-577A-95	Sequence 95, Appli	620	5.9	386	4	US-09-724-623-92	Sequence 92, Appli
549	62	6.0	911	3	US-08-448-194-6	Sequence 6, Appli	621	5.9	397	4	US-09-902-540-16267	Sequence 16267, A
550	62	6.0	911	3	US-08-613-009A-17	Sequence 17, Appli	622	5.9	402	3	US-09-134-001C-4674	Sequence 4674, Ap
551	62	6.0	911	3	US-08-897-438-95	Sequence 95, Appli	623	5.9	425	4	US-09-949-016-7395	Sequence 7395, Ap
552	62	6.0	911	3	US-08-867-921-6	Sequence 6, Appli	624	5.9	462	4	US-09-773-877B-18	Sequence 18, Appli
553	62	6.0	911	3	US-08-637-654-95	Sequence 95, Appli	625	5.9	478	3	US-09-570-454-2	Sequence 2, Appli
554	62	6.0	911	3	US-08-649-518-95	Sequence 95, Appli	626	5.9	478	4	US-09-867-521-2	Sequence 2, Appli
555	62	6.0	911	4	US-08-778-570B-23	Sequence 23, Appli	627	5.9	538	4	US-09-252-931A-22200	Sequence 22, Appli
556	62	6.0	911	4	US-09-059-584-23	Sequence 23, Appli	628	5.9	562	3	US-09-277-717-2	Sequence 22, Appli
557	62	6.0	915	1	US-08-487-890A-96	Sequence 96, Appli	629	5.9	562	3	US-09-173-151A-22	Sequence 12, Appli
558	62	6.0	915	2	US-08-363-124A-2	Sequence 2, Appli	630	5.9	567	4	US-09-773-877B-12	Sequence 12, Appli
559	62	6.0	915	2	US-08-478-435-96	Sequence 96, Appli	631	5.9	655	1	US-08-148-910-12	Sequence 12, Appli
560	62	6.0	915	2	US-08-337-483-96	Sequence 96, Appli	632	5.9	655	1	US-08-448-937A-12	Sequence 12, Appli
561	62	6.0	915	2	US-08-478-373-96	Sequence 96, Appli	633	5.9	659	4	US-09-710-279-1596	Sequence 1596, Ap
562	62	6.0	915	3	US-08-483-577A-96	Sequence 96, Appli	634	5.9	690	3	US-09-134-001C-4938	Sequence 4938, Ap
563	62	6.0	915	3	US-08-613-009A-18	Sequence 18, Appli	635	5.9	771	3	US-08-434-000A-8	Sequence 8, Appli
564	62	6.0	915	3	US-08-897-438-96	Sequence 96, Appli	636	5.9	771	3	US-09-312-157-8	Sequence 8, Appli
565	62	6.0	915	3	US-08-637-654-96	Sequence 96, Appli	637	5.9	771	4	US-09-717-888-8	Sequence 8, Appli
566	62	6.0	915	3	US-08-649-518-96	Sequence 96, Appli	638	5.9	883	4	US-09-270-767-44551	Sequence 44551, A
567	62	6.0	915	4	US-08-778-570B-24	Sequence 24, Appli	639	5.9	883	4	US-09-270-767-44907	Sequence 44907, A
568	62	6.0	915	4	US-09-059-584-24	Sequence 24, Appli	640	5.9	884	4	US-09-270-767-44755	Sequence 44755, A
569	62	6.0	917	4	US-08-753-750B-11	Sequence 11, Appli	641	5.9	979	3	US-08-878-474-5	Sequence 5, Appli
570	62	6.0	925	2	US-08-392-946-1	Sequence 1, Appli	642	5.9	981	4	US-09-902-540-9848	Sequence 9848, Ap
571	62	6.0	925	5	PCR-US94-14893-1	Sequence 1, Appli	643	5.9	1059	4	US-09-248-796A-15164	Sequence 15164, A
572	62	6.0	1019	1	US-08-296-014A-4	Sequence 4, Appli	644	5.9	2206	1	US-07-852-260-2	Sequence 2, Appli
573	62	6.0	1019	2	US-08-877-620-4	Sequence 4, Appli	645	5.9	2206	2	US-08-461-503-2	Sequence 2, Appli
574	62	6.0	1019	2	US-08-877-368-4	Sequence 4, Appli	646	5.9	2206	3	US-08-455-250-2	Sequence 2, Appli
575	62	6.0	1019	4	US-09-626-795-4	Sequence 4, Appli	647	5.9	67	4	US-09-328-352-5686	Sequence 5686, Ap
576	62	6.0	1042	3	US-08-928-361B-11	Sequence 11, Appli	648	5.9	67	4	US-09-919-039-202	Sequence 202, App
577	62	6.0	1042	3	US-08-588-995A-11	Sequence 11, Appli	649	5.9	107	1	US-08-425-336-125	Sequence 125, App
578	62	6.0	1083	1	US-08-296-014A-2	Sequence 2, Appli	650	5.9	107	1	US-08-488-113B-125	Sequence 125, App
579	62	6.0	1083	2	US-08-596-405-2	Sequence 2, Appli	651	5.9	107	1	US-08-477-484B-125	Sequence 125, App
580	62	6.0	1083	2	US-08-877-620-2	Sequence 2, Appli	652	5.9	107	1	US-08-107-669D-65	Sequence 65, Appli
581	62	6.0	1083	2	US-09-287-368-2	Sequence 2, Appli	653	5.9	107	1	US-08-477-531B-65	Sequence 65, Appli
582	62	6.0	1083	4	US-09-626-795-2	Sequence 2, Appli	654	5.9	107	2	US-08-646-360-125	Sequence 125, App
583	62	6.0	1837	3	US-08-928-361B-5	Sequence 5, Appli	655	5.9	107	2	US-08-477-484B-87	Sequence 87, Appli
584	62	6.0	2254	2	US-08-286-819A-28	Sequence 28, Appli	656	5.9	107	2	US-08-477-531B-65	Sequence 65, Appli
585	62	6.0	2254	3	US-08-980-357-28	Sequence 28, Appli	657	5.9	107	2	US-08-646-360-125	Sequence 125, App
586	62	6.0	2254	3	US-08-755-587-16	Sequence 16, Appli	658	5.9	107	2	US-08-839-765-125	Sequence 125, App
587	62	6.0	2254	3	US-09-976-594-726	Sequence 726, App	659	5.9	107	3	US-08-839-765-125	Sequence 125, App
588	62	6.0	2468	4	US-09-538-092-1135	Sequence 1135, Ap	660	5.9	107	3	US-09-136-389-125	Sequence 125, App
589	62	6.0	2468	4	US-09-949-016-10237	Sequence 10237, A	661	5.9	107	3	US-09-610-838-125	Sequence 125, App
590	62	6.0	2522	4	US-09-227-357-278	Sequence 278, A	662	5.9	109	4	US-09-711-485-125	Sequence 125, App
591	62	6.0	2522	4	US-08-630-822A-80	Sequence 80, Appli	663	5.9	227	1	US-09-802-083-3	Sequence 3, Appli
592	62	6.0	2522	4	US-09-005-069-58	Sequence 58, Appli	664	5.9	227	1	US-08-681-432-2	Sequence 2, Appli
593	61.5	5.9	46	3	US-09-005-069-58	Sequence 58, Appli	665	5.9	240	1	US-08-488-113B-148	Sequence 148, App
594	61.5	5.9	90	2	US-08-630-822A-80	Sequence 80, Appli	666	5.9	240	1	US-08-477-484B-148	Sequence 148, App
595	61.5	5.9	90	2	US-09-005-069-58	Sequence 58, Appli	667	5.9	240	1	US-08-646-360-148	Sequence 148, App
596	61.5	5.9	90	2	US-09-005-069-58	Sequence 58, Appli	668	5.9	240	3	US-08-839-765-148	Sequence 148, App
597	61.5	5.9	90	2	US-09-005-069-58	Sequence 58, Appli	669	5.9	240	3	US-09-136-389-148	Sequence 148, App
598	61.5	5.9	90	2	US-09-171-156A-12	Sequence 12, Appli	670	5.9	240	3	US-09-610-838-148	Sequence 148, App
599	61.5	5.9	90	3	US-09-171-156A-12	Sequence 12, Appli	671	5.9	269	4	US-09-711-485-148	Sequence 148, App
600	61.5	5.9	90	3	US-09-004-730A-12	Sequence 12, Appli	672	5.9	269	4	US-09-270-767-39555	Sequence 39555, A
601	61.5	5.9	90	4	US-09-004-730A-12	Sequence 12, Appli	673	5.9	269	4	US-09-270-767-54772	Sequence 54772, A
602	61.5	5.9	90	4	US-08-981-799A-12	Sequence 12, Appli	674	5.9	307	1	US-08-164-614A-11	Sequence 11, Appli
603	61.5	5.9	90	4	US-08-981-799A-14	Sequence 14, Appli	675	5.9	307	2	US-08-456-489B-11	Sequence 11, Appli
604	61.5	5.9	106	3	US-08-785-065-11	Sequence 11, Appli	676	5.9	313	4	US-09-489-039A-10034	Sequence 10034, A
605	61.5	5.9	106	3	US-09-151-412-11	Sequence 11, Appli	677	5.9	332	2	US-08-405-175A-5	Sequence 5, Appli
606	61.5	5.9	112	4	US-09-840-459-62	Sequence 62, Appli	678	5.9	360	4	US-09-454-071-4	Sequence 4, Appli
607	61.5	5.9	112	4	US-09-497-625A-62	Sequence 62, Appli	679	5.9	388	4	US-09-949-016-7331	Sequence 7331, Ap
608	61.5	5.9	131	2	US-08-850-910A-39	Sequence 39, Appli	680	5.9	400	4	US-09-420-819-37	Sequence 37, Appli
609	61.5	5.9	131	2	US-08-850-910A-41	Sequence 41, Appli	681	5.9	400	4	US-09-902-540-13370	Sequence 13370, A
610	61.5	5.9	131	2	US-08-850-910A-46	Sequence 46, Appli	682	5.9	401	4	US-09-420-819-36	Sequence 36, Appli
611	61.5	5.9	238	4	US-09-270-767-62179	Sequence 62179, A	683	5.9	419	4	US-09-949-016-6864	Sequence 6864, Ap
612	61.5	5.9	272	4	US-09-710-279-2290	Sequence 2290, Ap	684	5.9	433	4	US-09-248-796A-19799	Sequence 19799, A
							685	5.9	459	4	US-09-248-796A-19036	Sequence 19036, A
									466	4	US-09-949-016-7701	Sequence 7701, Ap

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687	61	5.9	522	2	US-08-456-489B-10	Sequence 10, Appl	760	60.5	5.8	370	4	US-09-540-236-2258	Sequence 2258, Ap
688	61	5.9	522	4	US-09-949-016-6185	Sequence 6185, Ap	761	60.5	5.8	376	3	US-08-711-417C-200	Sequence 200, Appl
689	61	5.9	530	4	US-09-252-991A-21963	Sequence 21963, A	762	60.5	5.8	376	4	US-08-733-622C-29	Sequence 29, Appl
690	61	5.9	536	1	US-08-164-614A-12	Sequence 12, Appl	763	60.5	5.8	376	3	US-09-723-909-200	Sequence 200, Appl
691	61	5.9	536	2	US-08-456-489B-12	Sequence 12, Appl	764	60.5	5.8	390	3	US-08-711-417C-199	Sequence 199, Appl
692	61	5.9	536	4	US-09-949-016-8560	Sequence 8560, Ap	765	60.5	5.8	390	4	US-08-733-622C-28	Sequence 28, Appl
693	61	5.9	560	2	US-08-808-931-18	Sequence 18, Appl	766	60.5	5.8	390	4	US-09-723-909-199	Sequence 199, Appl
694	61	5.9	560	3	US-08-808-323-18	Sequence 18, Appl	767	60.5	5.8	431	3	US-08-711-417C-195	Sequence 195, Appl
695	61	5.9	560	3	US-09-050-620A-18	Sequence 18, Appl	768	60.5	5.8	431	4	US-08-733-622C-24	Sequence 24, Appl
696	61	5.9	560	3	US-09-102-420B-18	Sequence 18, Appl	769	60.5	5.8	431	4	US-09-723-909-195	Sequence 195, Appl
697	61	5.9	560	3	US-09-497-698-18	Sequence 18, Appl	770	60.5	5.8	432	3	US-08-711-417C-197	Sequence 197, Appl
698	61	5.9	560	4	US-09-730-525-18	Sequence 18, Appl	771	60.5	5.8	432	3	US-08-733-622C-26	Sequence 26, Appl
699	61	5.9	644	1	US-08-487-890A-6	Sequence 6, Appl	772	60.5	5.8	432	4	US-09-723-909-197	Sequence 197, Appl
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701	61	5.9	644	2	US-08-337-483-6	Sequence 6, Appl	774	60.5	5.8	518	3	US-08-711-417C-198	Sequence 198, Appl
702	61	5.9	644	3	US-08-478-373-6	Sequence 6, Appl	775	60.5	5.8	518	4	US-08-733-622C-27	Sequence 27, Appl
703	61	5.9	644	3	US-08-474-671-6	Sequence 6, Appl	776	60.5	5.8	518	4	US-09-723-909-198	Sequence 198, Appl
704	61	5.9	644	3	US-08-483-577A-6	Sequence 6, Appl	777	60.5	5.8	527	4	US-09-270-767-45990	Sequence 45990, A
705	61	5.9	644	3	US-08-897-438-6	Sequence 6, Appl	778	60.5	5.8	554	3	US-08-462-467B-22	Sequence 22, Appl
706	61	5.9	644	3	US-08-637-654-6	Sequence 6, Appl	779	60.5	5.8	567	4	US-09-773-877B-35	Sequence 5, Appl
707	61	5.9	644	3	US-08-649-518-6	Sequence 6, Appl	780	60.5	5.8	568	5	PCT-US93-08743-5	Sequence 29, Appl
708	61	5.9	661	1	US-08-232-538-12	Sequence 12, Appl	781	60.5	5.8	577	2	US-07-728-215-29	Sequence 29, Appl
709	61	5.9	661	2	US-08-786-164-12	Sequence 12, Appl	782	60.5	5.8	577	3	US-08-938-085A-29	Sequence 29, Appl
710	61	5.9	672	4	US-09-252-991A-25389	Sequence 25389, A	783	60.5	5.8	577	4	US-10-072-844-29	Sequence 29, Appl
711	61	5.9	686	4	US-09-949-016-11203	Sequence 11203, A	784	60.5	5.8	577	4	US-10-072-838-29	Sequence 29, Appl
712	61	5.9	687	1	US-08-232-538-6	Sequence 6, Appl	785	60.5	5.8	577	4	US-10-072-841A-29	Sequence 29, Appl
713	61	5.9	687	2	US-08-786-164-6	Sequence 6, Appl	786	60.5	5.8	577	4	US-10-219-631A-29	Sequence 29, Appl
714	61	5.9	687	3	US-09-427-353-2	Sequence 2, Appl	787	60.5	5.8	600	4	US-09-270-767-42652	Sequence 42652, A
715	61	5.9	687	4	US-09-198-452A-848	Sequence 848, App	788	60.5	5.8	620	3	US-09-442-100-11	Sequence 11, Appl
716	61	5.9	687	4	US-09-438-185A-798	Sequence 798, App	789	60.5	5.8	620	4	US-08-939-106-11	Sequence 11, Appl
717	61	5.9	696	3	US-09-351-414-2	Sequence 2, Appl	790	60.5	5.8	620	4	US-09-442-102-11	Sequence 11, Appl
718	61	5.9	746	4	US-09-949-016-11494	Sequence 11494, A	791	60.5	5.8	652	2	US-08-751-305-2	Sequence 2, Appl
719	61	5.9	758	2	US-08-874-678-1	Sequence 1, Appl	792	60.5	5.8	782	1	US-07-725-083-2	Sequence 2, Appl
720	61	5.9	758	3	US-08-643-839-1	Sequence 1, Appl	793	60.5	5.8	782	3	US-08-669-286-10	Sequence 10, Appl
721	61	5.9	758	3	US-09-051-363-24	Sequence 24, Appl	794	60.5	5.8	782	3	US-09-469-253-10	Sequence 10, Appl
722	61	5.9	758	3	US-09-348-886-1	Sequence 1, Appl	795	60.5	5.8	782	3	US-09-642-146-10	Sequence 10, Appl
723	61	5.9	780	1	US-08-232-538-14	Sequence 14, Appl	796	60.5	5.8	787	4	US-09-949-016-9446	Sequence 9446, Ap
724	61	5.9	780	2	US-08-786-164-14	Sequence 14, Appl	797	60.5	5.8	915	4	US-09-252-991A-23779	Sequence 23779, A
725	61	5.9	832	4	US-09-634-252A-4	Sequence 4, Appl	798	60.5	5.8	1043	3	US-08-928-361B-30	Sequence 30, Appl
726	61	5.9	1338	3	US-08-750-014A-3	Sequence 3, Appl	799	60.5	5.8	1160	3	US-08-808-599A-24	Sequence 24, Appl
727	61	5.9	1338	4	US-09-119-014D-6	Sequence 6, Appl	800	60.5	5.8	1399	3	US-08-462-467B-14	Sequence 14, Appl
728	61	5.9	1362	2	US-08-874-678-33	Sequence 33, Appl	801	60.5	5.8	1721	3	US-08-700-651-5	Sequence 5, Appl
729	61	5.9	1362	3	US-08-643-839-33	Sequence 33, Appl	802	60.5	5.8	1721	3	US-08-928-361B-6	Sequence 6, Appl
730	61	5.9	1362	3	US-09-348-886-33	Sequence 33, Appl	803	60.5	5.8	1721	4	US-09-588-995A-6	Sequence 6, Appl
731	60.5	5.8	89	3	US-09-171-156A-53	Sequence 53, Appl	804	60.5	5.8	1826	4	US-09-198-452A-113	Sequence 113, App
732	60.5	5.8	89	4	US-09-004-730A-53	Sequence 53, Appl	805	60.5	5.8	1837	4	US-09-438-185A-98	Sequence 98, Appl
733	60.5	5.8	89	4	US-08-981-799A-53	Sequence 53, Appl	806	60.5	5.8	2756	1	US-08-375-709-11	Sequence 11, Appl
734	60.5	5.8	90	3	US-09-171-156A-56	Sequence 56, Appl	807	60.5	5.8	2756	1	US-08-752-929-11	Sequence 11, Appl
735	60.5	5.8	90	4	US-09-004-730A-56	Sequence 56, Appl	808	60.5	5.8	2756	3	US-09-090-793-7	Sequence 7, Appl
736	60.5	5.8	90	4	US-08-981-799A-56	Sequence 56, Appl	809	60.5	5.8	2756	4	US-09-231-899-7	Sequence 7, Appl
737	60.5	5.8	106	2	US-08-553-501A-84	Sequence 84, Appl	810	60	5.8	105	4	US-09-513-999C-5338	Sequence 5338, Ap
738	60.5	5.8	106	3	US-09-205-231-84	Sequence 84, Appl	811	60	5.8	124	4	US-09-640-211A-880	Sequence 880, App
739	60.5	5.8	123	4	US-09-462-606-59	Sequence 59, Appl	812	60	5.8	161	4	US-09-270-767-32081	Sequence 32081, A
740	60.5	5.8	126	2	US-08-553-501A-27	Sequence 27, Appl	813	60	5.8	161	4	US-09-270-767-47298	Sequence 47298, A
741	60.5	5.8	126	3	US-09-205-231-27	Sequence 27, Appl	814	60	5.8	162	1	US-08-031-399-5	Sequence 5, Appl
742	60.5	5.8	149	3	US-08-808-599A-40	Sequence 40, Appl	815	60	5.8	162	1	US-08-393-305-2	Sequence 2, Appl
743	60.5	5.8	208	2	US-08-606-143-40	Sequence 40, Appl	816	60	5.8	162	1	US-08-535-733-2	Sequence 2, Appl
744	60.5	5.8	214	1	US-08-458-516-12	Sequence 12, Appl	817	60	5.8	162	1	US-08-726-817-2	Sequence 2, Appl
745	60.5	5.8	230	4	US-09-252-991A-18556	Sequence 18556, A	818	60	5.8	162	1	US-08-504-042-5	Sequence 5, Appl
746	60.5	5.8	236	3	US-08-711-417C-174	Sequence 174, App	819	60	5.8	162	2	US-08-725-969-2	Sequence 2, Appl
747	60.5	5.8	236	4	US-09-723-909-174	Sequence 174, App	820	60	5.8	162	2	US-08-794-524-2	Sequence 2, Appl
748	60.5	5.8	236	4	US-09-270-767-41748	Sequence 41748, A	821	60	5.8	162	3	US-08-842-947-6	Sequence 6, Appl
749	60.5	5.8	236	4	US-09-902-540-11067	Sequence 11067, A	822	60	5.8	162	3	US-08-842-947-8	Sequence 8, Appl
750	60.5	5.8	244	3	US-08-772-440-2	Sequence 2, Appl	823	60	5.8	162	3	US-09-189-193-2	Sequence 2, Appl
751	60.5	5.8	261	4	US-09-270-767-32898	Sequence 32898, A	824	60	5.8	162	3	US-09-522-217-113	Sequence 113, App
752	60.5	5.8	261	4	US-09-270-767-48115	Sequence 48115, A	825	60	5.8	162	4	US-09-437-585-6	Sequence 6, Appl
753	60.5	5.8	285	3	US-09-318-661-4	Sequence 4, Appl	826	60	5.8	162	4	US-09-437-585-8	Sequence 8, Appl
754	60.5	5.8	285	4	US-09-883-758-4	Sequence 4, Appl	827	60	5.8	162	4	US-09-923-246-113	Sequence 113, App
755	60.5	5.8	329	3	US-09-413-231-5	Sequence 5, Appl	828	60	5.8	162	4	US-10-295-723-113	Sequence 113, App
756	60.5	5.8	329	3	US-09-413-231-9	Sequence 9, Appl	829	60	5.8	162	4	US-09-855-313A-2	Sequence 2, Appl
757	60.5	5.8	348	1	US-08-468-847B-14	Sequence 14, Appl	830	60	5.8	162	4	US-09-855-313A-4	Sequence 4, Appl
758	60.5	5.8	349	3	US-08-462-467B-18	Sequence 18, Appl	831	60	5.8	162	4	US-09-949-016-5964	Sequence 5964, Ap

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833	60	5.8	162	5	PCT-US96-06423-2	Sequence 2, Appli	906	59.5	5.7	232	4	US-08-733-622C-31	Sequence 31, Appl
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835	60	5.8	180	4	US-09-461-688-4	Sequence 4, Appli	908	59.5	5.7	304	4	US-09-685-166A-835	Sequence 835, App
836	60	5.8	218	4	US-09-698-705-12	Sequence 12, Appl	909	59.5	5.7	304	4	US-09-679-426-835	Sequence 835, App
837	60	5.8	219	1	US-08-461-005-13	Sequence 13, Appl	910	59.5	5.7	304	4	US-09-759-143-835	Sequence 835, App
838	60	5.8	219	2	US-07-930-685-13	Sequence 13, Appl	911	59.5	5.7	304	4	US-09-651-236-835	Sequence 835, App
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840	60	5.8	301	3	US-09-217-847-25	Sequence 25, Appl	913	59.5	5.7	327	3	US-09-008-271A-10	Sequence 10, Appl
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843	60	5.8	349	1	US-08-386-680-2	Sequence 2, Appli	916	59.5	5.7	341	3	US-08-949-202-4	Sequence 2, Appli
844	60	5.8	349	1	US-08-459-717-2	Sequence 2, Appli	917	59.5	5.7	341	3	US-08-949-202-4	Sequence 4, Appli
845	60	5.8	349	1	US-08-712-302-2	Sequence 2, Appli	918	59.5	5.7	341	3	US-09-418-175-2	Sequence 2, Appli
846	60	5.8	349	2	US-08-880-031-2	Sequence 2, Appli	919	59.5	5.7	341	3	US-09-418-175-2	Sequence 2, Appli
847	60	5.8	349	3	US-09-054-368-2	Sequence 2, Appli	920	59.5	5.7	341	4	US-09-529-245-2	Sequence 2, Appli
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851	60	5.8	349	3	US-09-056-704-2	Sequence 2, Appli	924	59.5	5.7	386	4	US-09-270-767-44120	Sequence 44120, A
852	60	5.8	349	3	US-09-292-036-4	Sequence 4, Appli	925	59.5	5.7	410	1	US-07-945-283-4	Sequence 4, Appli
853	60	5.8	349	3	US-09-253-316-26	Sequence 26, Appl	926	59.5	5.7	445	4	US-09-248-796A-17188	Sequence 17188, A
854	60	5.8	349	4	US-09-142-569-8	Sequence 8, Appli	927	59.5	5.7	452	4	US-09-902-540-15423	Sequence 15423, A
855	60	5.8	349	4	US-09-461-688-2	Sequence 8, Appli	928	59.5	5.7	490	4	US-09-252-991A-21383	Sequence 21383, A
856	60	5.8	349	4	US-09-495-448A-8	Sequence 8, Appli	929	59.5	5.7	494	3	US-08-993-260-3	Sequence 3, Appli
857	60	5.8	349	4	US-09-949-016-6141	Sequence 6141, Ap	930	59.5	5.7	530	4	US-09-252-991A-23952	Sequence 23952, A
858	60	5.8	349	5	PCT-US96-08140-2	Sequence 2, Appli	931	59.5	5.7	538	4	US-09-616-289-43	Sequence 43, Appl
859	60	5.8	414	4	US-09-640-211A-2247	Sequence 2247, Ap	932	59.5	5.7	596	4	US-09-134-000C-6209	Sequence 6209, Ap
860	60	5.8	432	4	US-09-170-984-10	Sequence 10, Appl	933	59.5	5.7	638	4	US-09-252-991A-22490	Sequence 22490, A
861	60	5.8	453	4	US-09-949-016-10252	Sequence 10252, A	934	59.5	5.7	738	6	Patent No. 5264554	Patent No. 5264554
862	60	5.8	468	4	US-09-270-767-44250	Sequence 44250, A	935	59.5	5.7	738	6	Patent No. 5264554-2	Patent No. 5264554
863	60	5.8	488	4	US-09-248-796A-20028	Sequence 20028, A	936	59.5	5.7	741	4	US-09-270-767-41593	Sequence 41593, A
864	60	5.8	489	4	US-09-252-991A-16940	Sequence 16940, A	937	59.5	5.7	770	1	US-08-369-796-12	Sequence 12, Appl
865	60	5.8	514	4	US-09-252-991A-18306	Sequence 18306, A	938	59.5	5.7	770	1	US-08-416-581B-1	Sequence 1, Appli
866	60	5.8	515	4	US-10-037-667-4	Sequence 4, Appli	939	59.5	5.7	770	1	US-08-416-581B-5	Sequence 5, Appli
867	60	5.8	523	3	US-09-302-620B-95	Sequence 95, Appl	940	59.5	5.7	770	1	US-08-416-581B-9	Sequence 9, Appli
868	60	5.8	579	3	US-08-704-711A-1	Sequence 1, Appli	941	59.5	5.7	770	2	US-08-852-091-12	Sequence 12, Appl
869	60	5.8	582	3	US-09-521-220-1	Sequence 1, Appli	942	59.5	5.7	770	2	US-08-820-754-12	Sequence 12, Appl
870	60	5.8	582	3	US-08-448-489-1	Sequence 2, Appli	943	59.5	5.7	770	2	US-08-956-652-12	Sequence 12, Appl
871	60	5.8	582	3	US-08-704-711A-2	Sequence 2, Appli	944	59.5	5.7	770	3	US-08-956-652-12	Sequence 12, Appl
872	60	5.8	582	3	US-09-211-704A-9	Sequence 9, Appli	945	59.5	5.7	770	3	US-08-956-652-12	Sequence 12, Appl
873	60	5.8	582	3	US-09-521-220-2	Sequence 2, Appli	946	59.5	5.7	770	3	US-08-956-652-12	Sequence 12, Appl
874	60	5.8	582	3	US-09-391-104-28	Sequence 28, Appl	947	59.5	5.7	770	3	US-08-956-652-12	Sequence 12, Appl
875	60	5.8	582	4	US-09-919-497-84	Sequence 84, Appl	948	59.5	5.7	770	3	US-08-948-547-12	Sequence 12, Appl
876	60	5.8	582	4	US-09-689-730-1	Sequence 1, Appli	949	59.5	5.7	770	3	US-09-364-970-3	Sequence 3, Appli
877	60	5.8	614	4	US-09-328-352-5476	Sequence 5476, Ap	950	59.5	5.7	770	3	US-09-364-970-5	Sequence 5, Appli
878	60	5.8	619	3	US-09-423-890-4	Sequence 4, Appli	951	59.5	5.7	770	3	US-09-556-273-8	Sequence 8, Appli
879	60	5.8	630	3	US-09-342-647-2	Sequence 2, Appli	952	59.5	5.7	770	3	US-08-956-653A-12	Sequence 12, Appl
880	60	5.8	631	4	US-09-620-412C-325	Sequence 325, App	953	59.5	5.7	770	3	US-09-526-542-2	Sequence 2, Appli
881	60	5.8	631	4	US-09-598-419-325	Sequence 325, App	954	59.5	5.7	770	4	US-08-212-185-12	Sequence 12, Appl
882	60	5.8	656	3	US-09-134-001C-4322	Sequence 4322, Ap	955	59.5	5.7	770	4	US-10-117-087-2	Sequence 2, Appli
883	60	5.8	668	4	US-09-252-991A-22341	Sequence 22341, A	956	59.5	5.7	770	5	PCT-US95-17025-12	Sequence 12, Appl
884	60	5.8	717	4	US-09-881-578A-2	Sequence 2, Appli	957	59.5	5.7	771	1	US-08-276-899A-14	Sequence 14, Appl
885	60	5.8	804	4	US-09-328-352-5545	Sequence 5545, Ap	958	59.5	5.7	771	1	US-08-781-890-14	Sequence 14, Appl
886	60	5.8	823	4	US-09-538-092-439	Sequence 439, App	959	59.5	5.7	788	3	US-07-728-215-27	Sequence 27, Appl
887	60	5.8	924	1	US-08-481-130-28	Sequence 28, Appl	960	59.5	5.7	788	3	US-08-938-085A-27	Sequence 27, Appl
888	60	5.8	924	1	US-08-656-984A-28	Sequence 28, Appl	961	59.5	5.7	788	4	US-10-072-844-27	Sequence 27, Appl
889	60	5.8	924	2	US-08-485-604-28	Sequence 28, Appl	962	59.5	5.7	788	4	US-10-072-844-27	Sequence 27, Appl
890	60	5.8	924	2	US-08-487-595-28	Sequence 28, Appl	963	59.5	5.7	788	4	US-10-072-844A-27	Sequence 27, Appl
891	60	5.8	940	4	US-09-198-452A-111	Sequence 111, App	964	59.5	5.7	788	4	US-10-219-631A-27	Sequence 27, Appl
892	60	5.8	956	4	US-09-438-185A-96	Sequence 96, Appl	965	59.5	5.7	794	4	US-09-949-016-6714	Sequence 6714, Ap
893	60	5.8	1192	4	US-09-560-385A-34	Sequence 34, Appl	966	59.5	5.7	812	4	US-09-949-016-10746	Sequence 10746, A
894	60	5.8	1380	4	US-09-949-016-11688	Sequence 11688, A	967	59.5	5.7	812	4	US-09-949-016-11435	Sequence 11435, A
895	60	5.8	1704	4	US-09-392-812A-2	Sequence 2, Appli	968	59.5	5.7	903	1	US-08-220-151-8	Sequence 8, Appli
896	59.5	5.7	66	4	US-09-328-352-5756	Sequence 5756, Ap	969	59.5	5.7	903	1	US-08-413-118-8	Sequence 8, Appli
897	59.5	5.7	166	4	US-09-328-352-6145	Sequence 6145, Ap	970	59.5	5.7	903	3	US-08-473-446-8	Sequence 8, Appli
898	59.5	5.7	183	4	US-09-328-352-6145	Sequence 31093, A	971	59.5	5.7	942	4	US-10-101-464A-911	Sequence 911, App
899	59.5	5.7	184	4	US-09-270-767-31979	Sequence 31979, A	972	59.5	5.7	1207	4	US-09-328-352-6766	Sequence 6766, App
900	59.5	5.7	184	4	US-09-270-767-47196	Sequence 47196, A	973	59.5	5.7	1221	4	US-09-107-532A-3959	Sequence 3959, Ap
901	59.5	5.7	203	4	US-09-640-211A-1068	Sequence 1068, Ap	974	59.5	5.7	1251	4	US-09-252-991A-17263	Sequence 17263, A
902	59.5	5.7	215	2	US-08-480-753-8	Sequence 8, Appli	975	59.5	5.7	1876	2	US-08-603-049A-12	Sequence 12, Appl
903	59.5	5.7	217	3	US-08-979-608A-7	Sequence 7, Appli	976	59.5	5.7	1876	3	US-09-170-996-12	Sequence 12, Appl
904	59.5	5.7	217	4	US-09-517-849-7	Sequence 7, Appli	977	59.5	5.7	3730	4	US-09-949-016-9908	Sequence 9908, Ap

978	59	5.7	154	4	US-09-270-767-46156	Sequence 46156, A	1051	5.6	513	3	US-08-889-419-19	Sequence 19, Appl
979	59	5.7	154	4	US-09-902-540-12436	Sequence 12436, A	1052	5.6	513	3	US-08-469-411-8	Sequence 8, Appl
980	59	5.7	198	4	US-09-270-767-46090	Sequence 46090, A	1053	5.6	513	3	US-08-402-542-19	Sequence 19, Appl
981	59	5.7	221	4	US-09-949-016-10154	Sequence 10154, A	1054	5.6	513	4	US-09-780-601A-8	Sequence 8, Appl
982	59	5.7	232	4	US-09-252-991A-27530	Sequence 27530, A	1055	5.6	513	4	US-09-949-016-6118	Sequence 6118, Ap
983	59	5.7	238	3	US-09-192-545-4	Sequence 4, Appl	1056	5.6	513	5	PCT-US93-07189-19	Sequence 19, Appl
984	59	5.7	241	4	US-09-248-796A-17889	Sequence 17889, A	1057	5.6	513	6	5187076-6	Patent No. 5187076
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986	59	5.7	278	3	US-08-852-401-4	Sequence 4, Appl	1059	5.6	516	3	US-08-711-417C-202	Sequence 202, App
987	59	5.7	326	4	US-09-328-352-5506	Sequence 5506, Ap	1060	5.6	516	4	US-09-723-909-202	Sequence 202, App
988	59	5.7	329	2	US-08-739-485-3	Sequence 3, Appl	1061	5.6	521	4	US-09-949-016-11081	Sequence 11081, A
989	59	5.7	338	4	US-09-489-039A-12432	Sequence 12432, A	1062	5.6	521	4	US-09-949-016-11082	Sequence 11082, A
990	59	5.7	361	4	US-09-282-931A-32937	Sequence 32937, A	1063	5.6	521	4	US-09-949-016-11083	Sequence 11083, A
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992	59	5.7	469	4	US-09-347-650-16	Sequence 16, Appl	1065	5.6	543	1	US-08-814-196-2	Sequence 2, Appl
993	59	5.7	469	4	US-09-291-023A-18	Sequence 18, Appl	1066	5.6	559	4	US-09-583-110-3735	Sequence 3735, Ap
994	59	5.7	485	4	US-09-381-687-1	Sequence 1, Appl	1067	5.6	563	3	US-08-362-525-12	Sequence 12, Appl
995	59	5.7	485	4	US-09-540-715A-18	Sequence 18, Appl	1068	5.6	563	3	US-09-949-016-11259	Sequence 11259, A
996	59	5.7	492	4	US-09-252-991A-30857	Sequence 30857, A	1069	5.6	567	4	US-09-107-433-4592	Sequence 4592, Ap
997	59	5.7	493	4	US-08-543-681A-7006	Sequence 7006, Ap	1070	5.6	608	4	US-09-248-796A-20178	Sequence 20178, A
998	59	5.7	505	4	US-09-489-039A-9945	Sequence 9945, Ap	1071	5.6	635	4	US-09-417-197-125	Sequence 125, App
999	59	5.7	516	4	US-09-986-676A-2	Sequence 2, Appl	1072	5.6	685	4	US-09-252-991A-32033	Sequence 32033, A
1000	59	5.7	516	4	US-09-971-611-2	Sequence 2, Appl	1073	5.6	690	4	US-09-538-092-294	Sequence 294, A
1001	59	5.7	587	4	US-09-252-991A-18280	Sequence 18280, A	1074	5.6	691	3	US-08-946-475-2	Sequence 2, Appl
1002	59	5.7	599	4	US-10-101-464A-904	Sequence 904, App	1075	5.6	691	3	US-08-946-475-2	Sequence 2, Appl
1003	59	5.7	604	4	US-09-902-540-12446	Sequence 12446, A	1076	5.6	711	3	US-09-340-479-9	Sequence 9, Appl
1004	59	5.7	774	3	US-09-276-400-7	Sequence 7, Appl	1077	5.6	711	3	US-09-902-540-11385	Sequence 11385, A
1005	59	5.7	774	3	US-09-448-076-7	Sequence 7, Appl	1078	5.6	718	4	US-08-478-208-32	Sequence 32, Appl
1006	59	5.7	774	3	US-09-702-572-7	Sequence 7, Appl	1079	5.6	738	3	US-09-336-536-73	Sequence 73, Appl
1007	59	5.7	825	4	US-10-210-428-1	Sequence 1, Appl	1080	5.6	738	4	US-09-583-110-3066	Sequence 3066, Ap
1008	59	5.7	825	4	US-10-237-551-161	Sequence 161, App	1081	5.6	747	4	US-09-107-433-3375	Sequence 3375, Ap
1009	59	5.7	826	4	US-09-894-998A-47	Sequence 47, Appl	1082	5.6	751	4	US-08-942-686-2	Sequence 2, Appl
1010	59	5.7	826	4	US-10-237-551-47	Sequence 47, Appl	1083	5.6	777	4	US-09-270-767-44409	Sequence 44409, A
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1012	59	5.7	2362	4	US-09-949-016-8985	Sequence 8985, Ap	1085	5.6	847	4	US-10-162-012-2	Sequence 2, Appl
1013	59	5.7	4544	1	US-08-469-486-52	Sequence 52, Appl	1086	5.6	849	4	US-09-081-385-152	Sequence 152, App
1014	59	5.7	4544	2	US-08-469-658-52	Sequence 52, Appl	1087	5.6	849	4	US-09-438-185A-473	Sequence 473, App
1015	59	5.6	114	4	US-09-270-767-57487	Sequence 57487, A	1088	5.6	947	3	US-08-545-860D-55	Sequence 55, Appl
1016	59	5.6	142	4	US-09-640-211A-886	Sequence 886, App	1089	5.6	1033	5	PCT-US94-04496-55	Sequence 55, Appl
1017	59	5.6	145	4	US-09-252-991A-27732	Sequence 27732, A	1090	5.6	1093	5	US-09-949-016-10194	Sequence 10194, A
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1019	59	5.6	208	4	US-09-252-991A-25609	Sequence 25609, A	1092	5.6	1170	1	US-09-657-472-2	Sequence 2, Appl
1020	59	5.6	236	3	US-08-711-417C-175	Sequence 175, App	1093	5.6	1170	4	US-09-309-572-7	Sequence 7, Appl
1021	59	5.6	236	3	US-09-723-909-175	Sequence 175, App	1094	5.6	2210	4	US-09-718-096-7	Sequence 7, Appl
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1023	59	5.6	283	1	US-08-726-227-4	Sequence 4, Appl	1096	5.6	2491	4	US-09-150-867-1	Sequence 1, Appl
1024	59	5.6	283	3	US-08-826-246-6	Sequence 6, Appl	1097	5.6	2954	4	US-08-222-719-4	Sequence 4, Appl
1025	59	5.6	283	3	US-08-944-495-6	Sequence 6, Appl	1098	5.6	122	2	US-08-470-925-4	Sequence 4, Appl
1026	59	5.6	283	3	US-09-126-640-9	Sequence 9, Appl	1099	5.6	122	2	US-08-471-613-4	Sequence 4, Appl
1027	59	5.6	283	3	US-08-925-588-6	Sequence 6, Appl	1100	5.6	122	2	PCT-US93-10443-4	Sequence 36819, A
1028	59	5.6	283	3	US-09-288-292A-9	Sequence 9, Appl	1101	5.6	141	4	US-09-270-767-36819	Sequence 52036, A
1029	59	5.6	283	4	US-09-372-044-6	Sequence 6, Appl	1102	5.6	141	4	US-08-318-193-14	Sequence 14, Appl
1030	59	5.6	283	4	US-08-825-486-6	Sequence 6, Appl	1103	5.6	146	1	US-08-232-087A-11	Sequence 11, Appl
1031	59	5.6	283	4	US-08-826-248-6	Sequence 6, Appl	1104	5.6	159	2	US-08-222-719-3	Sequence 3, Appl
1032	59	5.6	294	3	US-09-518-046-4	Sequence 4, Appl	1105	5.6	185	2	US-08-470-925-3	Sequence 3, Appl
1033	59	5.6	334	3	US-08-711-417C-201	Sequence 201, App	1106	5.6	185	2	US-08-471-613-3	Sequence 3, Appl
1034	59	5.6	334	4	US-08-733-622C-23	Sequence 23, Appl	1107	5.6	185	2	PCT-US93-10443-3	Sequence 10754, A
1035	59	5.6	334	4	US-09-723-909-201	Sequence 201, App	1108	5.6	226	4	US-09-489-039A-10754	Sequence 514, App
1036	59	5.6	352	4	US-09-270-767-42211	Sequence 42211, A	1109	5.6	328	4	US-09-538-092-514	Sequence 4175, Ap
1037	59	5.6	353	4	US-09-107-532A-7032	Sequence 7032, Ap	1110	5.6	404	4	US-09-328-352-4175	Sequence 13003, A
1038	59	5.6	355	2	US-08-458-555-2	Sequence 2, Appl	1111	5.6	434	4	US-09-902-540-13003	Sequence 38, Appl
1039	59	5.6	382	4	US-09-248-796A-17276	Sequence 17276, A	1112	5.6	445	3	US-08-845-258-38	Sequence 38, Appl
1040	59	5.6	390	4	US-09-543-681A-5753	Sequence 5753, Ap	1113	5.6	445	3	US-08-990-571-38	Sequence 38, Appl
1041	59	5.6	410	4	US-09-489-039A-11862	Sequence 11862, A	1114	5.6	445	3	US-08-723-142A-38	Sequence 38, Appl
1042	59	5.6	437	3	US-09-353-332-2	Sequence 2, Appl	1115	5.6	445	3	US-09-528-784A-38	Sequence 38, Appl
1043	59	5.6	454	3	US-09-518-046-2	Sequence 2, Appl	1116	5.6	445	3	US-09-569-098A-38	Sequence 38, Appl
1044	59	5.6	455	3	US-09-261-416-2	Sequence 2, Appl	1117	5.6	445	4	US-09-902-540-16449	Sequence 29798, A
1045	59	5.6	461	3	US-08-711-417C-196	Sequence 196, App	1118	5.6	445	4	US-09-438-185A-872	Sequence 872, App
1046	59	5.6	461	4	US-08-733-622C-25	Sequence 25, Appl	1119	5.6	457	4	US-09-112-498A-2	Sequence 2, Appl
1047	59	5.6	461	4	US-09-723-909-196	Sequence 196, App	1120	5.6	493	4	US-09-413-814-88	Sequence 88, Appl
1048	59	5.6	472	2	US-08-811-949-63	Sequence 63, Appl	1121	5.6	493	4		
1049	59	5.6	513	2	US-08-459-346-19	Sequence 19, Appl	1122	5.6	493	4		
1050	59	5.6	513	2	US-07-989-847-8	Sequence 8, Appl	1123	5.6	494	3		

1124	58	5.6	496	4	US-09-800-170-20	Sequence 20, Appl	1197	57.5	5.6	100	4	US-09-472-087-113	Sequence 113, Appl
1125	58	5.6	506	4	US-09-370-838-34	Sequence 34, Appl	1198	57.5	5.6	111	1	US-07-942-245-29	Sequence 29, Appl
1126	58	5.6	506	4	US-09-854-133-34	Sequence 34, Appl	1199	57.5	5.6	111	1	US-08-477-877B-89	Sequence 89, Appl
1127	58	5.6	552	4	US-09-460-295B-8	Sequence 8, Appl	1200	57.5	5.6	112	2	US-08-472-281A-89	Sequence 89, Appl
1128	58	5.6	569	4	US-09-137-223A-3	Sequence 3, Appl	1201	57.5	5.6	112	2	US-08-477-989B-89	Sequence 89, Appl
1129	58	5.6	574	1	US-08-049-473A-2	Sequence 2, Appl	1202	57.5	5.6	112	4	US-09-840-459-35	Sequence 55, Appl
1130	58	5.6	574	1	US-08-312-648-2	Sequence 2, Appl	1203	57.5	5.6	112	4	US-09-840-459-66	Sequence 66, Appl
1131	58	5.6	574	5	PCT-US94-04190-2	Sequence 2, Appl	1204	57.5	5.6	112	4	US-09-497-625A-55	Sequence 55, Appl
1132	58	5.6	581	4	US-09-949-016-11632	Sequence 11632, A	1205	57.5	5.6	112	4	US-09-497-625A-66	Sequence 66, Appl
1133	58	5.6	584	4	US-09-252-991A-18292	Sequence 18292, A	1206	57.5	5.6	112	4	US-09-254-180C-8	Sequence 8, Appl
1134	58	5.6	602	3	US-08-990-470A-3	Sequence 3, Appl	1207	57.5	5.6	123	4	US-09-462-606-58	Sequence 58, Appl
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1136	58	5.6	603	4	US-09-906-779-4	Sequence 4, Appl	1209	57.5	5.6	124	1	US-08-240-049B-20	Sequence 20, Appl
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1342	57	5.5	242	3	US-09-027-449-51	Sequence 51, Appl	1424	57	5.5				


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Qy 145 IFDGGPRPTGKRYCINSAALSFTPADSSGTAEGGVSAPQAADKAE 191
Db 151 VFEDGPKTRKRYCINSASIEFVNAD---PATSSPPVAITPAPIAQ 194

RESULT 3
US-09-543-681A-8198
; Sequence 8198, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 8198
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-8198

Query Match 39.5%; Score 409.5; DB 4; Length 164;
Best Local Similarity 45.6%; Pred. No. 1.5e-38;
Matches 72; Conservative 30; Mismatches 41; Indels 15; Gaps 2;

Qy 35 CRDKKN---CKVVFSSQELR-----KRLTPLYHVHTQEKGTESAFEGEYTHHK 79
Db 7 CCFKKHFCQCEVFMNNEKKVHISDDNHIDLSNLENMCHVYTOQRGTEPPFSKLLHNR 66

Qy 80 DPGIYKVCVCGTPLFKSTKFDGSGWPSFHDVINSEAITTDDFSYGMHRVETSCQCG 139
Db 67 ETGIYHCLCCSAPLFYSYSETKDAGCGWPSFQPVSDDAIYLDLDFSHNMKRTIRCHQCG 126

Qy 140 AHLGHIFDGGPRPTGKRYCINSAALSFTPADSSGTAEG 177
Db 127 AHLGHVNDGPAPTGQRYCVNSASLAFSNTGEVQKG 164

RESULT 4
US-09-489-039A-7828
; Sequence 7828, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7828
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7828

Query Match 39.2%; Score 406.5; DB 4; Length 155;
Best Local Similarity 49.0%; Pred. No. 3e-38;
Matches 70; Conservative 29; Mismatches 41; Indels 3; Gaps 1;

Qy 38 KKNCKVVFSSQ---QSLRKRLTPLYHVHTQEKGTESAFEGEYTHHKDPGIYKVCVCGTPLF 94
Db 13 KARCKPMANKPTPEELKKNGLSMDQFYVTHHGTEPPFTGRLLHNKNGVYICLVCDAPLF 72

Qy 95 KSETKFDGSGWPSFHDVINSEAITTDDFSYGMHRVETSCQCGAHLGHIFDGGPRPTG 154
Db 73 NSQTKYDSCGCGWPSFYPVSAEIRYLTDSHGMQRIEIRCNCDALHGHVFPDGPQPTG 132
```

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Qy 155 KRYCINSAALSFTPADSSGTAEG 177
Db 133 ERYCVNSASLSFTDEQNGEQIKG 155

RESULT 5
US-09-252-991A-26314
; Sequence 26314, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26314
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26314

Query Match 39.2%; Score 406.5; DB 4; Length 186;
Best Local Similarity 50.3%; Pred. No. 3.9e-38;
Matches 74; Conservative 21; Mismatches 49; Indels 3; Gaps 1;

Qy 28 GSAQSGSCRDKK---NCKVVFSSQELRKRLTPLYHVHTQEKGTESAFEGEYTHHKDPGIY 84
Db 40 GKSAGHFSREVEPMSKIDKPLDSWREELTBSQFHICRLGGTERAFSGETHATKTPGIY 99

Qy 85 KCVVCGTPLFKSTKFDGSGWPSFHDVINSEAITTDDFSYGMHRVETSCQCGAHLGH 144
Db 100 HCTCCGTALFDSDAKYDGSWGWSYFQPDAAEAVRELLDDFSHGMHREVCRCDAHLGH 159

Qy 145 IFDGGPRPTGKRYCINSAALSFTPADS 171
Db 160 VFDPGPRPTGLRYCINSASLKLVPRES 186

RESULT 6
US-09-640-211A-735
; Sequence 735, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Transcription
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 735
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-09-640-211A-735

Query Match 33.6%; Score 348.5; DB 4; Length 133;
Best Local Similarity 52.6%; Pred. No. 9.8e-32;
Matches 70; Conservative 15; Mismatches 45; Indels 3; Gaps 1;

Qy 27 LGSAQSGSCRDKKCK---VVFSSQELRKRLTPLYHVHTQEKGTESAFEGEYTHHKDPGI 83
Db 133 ERYCVNSASLSFTDEQNGEQIKG 155
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Db 1 MGSSASSORPNLQDKVGPVSDEWKKRLTPEQYYVARQKGTERTAFSGYWNKTPGT 60

Qy 84 YKVCVCGTPLFKSETKPDGSGWPSFHDVINSEAITFTDDFSYGMHRVETSCSOGCAHLG 143

Db 61 YHVCDDTPLFESNTKFDGSGWPSYQPIGNVKSCLDLIIFMPROEVLCAACDAHLG 120

Qy 144 HIFDDGPRPTGKR 156

Db 121 HIFDDGPPPTGKR 133

RESULT 7

US-09-328-352-6906

; Sequence 6906, Application US/09328352

; Patent No. 6562958

; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC99-03PA

; CURRENT APPLICATION NUMBER: US/09/328,352

; CURRENT FILING DATE: 1999-06-04

; NUMBER OF SEQ ID NOS: 8252

; SEQ ID NO 6906

; LENGTH: 143

; TYPE: PRT

; ORGANISM: Acinetobacter baumannii

US-09-328-352-6906

Query Match 33.6%; Score 348; DB 4; Length 143;

Best Local Similarity 49.6%; Pred. No. 1.2e-31;

Matches 61; Conservative 22; Mismatches 40; Indels 0; Gaps 0;

Qy 42 KVFSSQQLRLKRLTLPLOYHVTQKTESAFEGEYTHHKDPGIYKVCVCGTPLFKSETKFD 101

Db 7 KVNKTREWQRELSPEYRITRKQTEPAFTQYWNKQHGTYVCRCCGALFSSDAKYD 66

Qy 102 SSGSWPSFHDVINSEAITFTDDFSYGMHRVETSCSOGCAHLGHIFFDDGPRPTGKRYCINS 161

Db 67 SCGWPSFPRPLNGSVIDHEDLTHGMVTEIVCHDCEAHLGHVFDGPOPTGLRYCINS 126

Qy 162 AAL 164

Db 127 ASL 129

RESULT 8

US-09-902-540-11587

; Sequence 11587, Application US/09902540

; Patent No. 6833447

; GENERAL INFORMATION:

; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Wiegand, Roger C.

; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

; FILE REFERENCE: 38-10(15849)B

; CURRENT APPLICATION NUMBER: US/09/902,540

; CURRENT FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: 60/217,883

; PRIOR FILING DATE: 2000-07-10

; NUMBER OF SEQ ID NOS: 16825

; SEQ ID NO 11587

; LENGTH: 357

; TYPE: PRT

; ORGANISM: Myxococcus xanthus

US-09-902-540-11587

Query Match 32.0%; Score 332; DB 4; Length 357;

Best Local Similarity 40.7%; Pred. No. 3.1e-29;

Matches 77; Conservative 23; Mismatches 81; Indels 8; Gaps 3;

Qy 10 PLSLCLSLCLCLAA--ALGSAQSGSCRDKNCKVVFSSQQLRLKRLTLPLOYHVTQKGT 67

Db 2 PLALAAVLVSACTEARGAAPGPTIQDTRRYEKP-SDADLRRTLSPLAYEVTQKAT 60

Qy 68 ESAFEGEYTHHKDPGIYKVCVCGTPLFKSETKPDGSGWPSFHDVINSEAITFTDDFSYG 127

Db 61 EPAFRNLWNHHEGLYDVVVGSEPLFSSRDKPDGSGWPSFTRPVD SARIVEKRDSIQ 120

Qy 128 MHRVETSCSOGCAHLGHIFFDDGPRPTGKRYCINSAAALSFPPADSSGTABGGS-----GVA 182

Db 121 MERVESKKAAGSHLFGDPAPAKTRYCINSAAALRFVAVNDLAKEGYGAWLPLFRP 180

Qy 183 SPAQADKAE 191

Db 181 APAATKRQ 189

RESULT 9

US-09-540-236-2621

; Sequence 2621, Application US/09540236

; Patent No. 6673910

; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR

; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709.2005-001

; CURRENT APPLICATION NUMBER: US/09/540,236

; CURRENT FILING DATE: 2000-04-04

; NUMBER OF SEQ ID NOS: 3840

; SEQ ID NO 2621

; LENGTH: 138

; TYPE: PRT

; ORGANISM: M.catarrhalis

US-09-540-236-2621

Query Match 31.0%; Score 321.5; DB 4; Length 138;

Best Local Similarity 51.7%; Pred. No. 1.2e-28;

Matches 62; Conservative 14; Mismatches 43; Indels 1; Gaps 1;

Qy 46 SQQLRLKRLTLPLOYHVTQKTESAFEGEYTHHKDPGIYKVCVCGTPLFKSETKPDGSG 105

Db 14 SEADQNRLDLSYVLRQKTEQAFTGLYTDTEVEGIYRCKGCHTLPDSSAKFHSKCG 73

Qy 106 WPSFHDVINSEAITFTDDFSYGMHRVETSCSOGCAHLGHIFFDDG-PRTGKRYCINSAA 164

Db 74 WPSFKVIADNVVDVETLDSLHGMRIEVTCHCGHLGHVFPDNYVYTDTLGRLYCINSA 133

RESULT 10

US-09-134-001C-3135

; Sequence 3135, Application US/09134001C

; Patent No. 6380370

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134,001C

; CURRENT FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: US 60/055,779

; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 3135

; LENGTH: 154

; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-3135

Query Match 29.3%; Score 303.5; DB 3; Length 154;

Best Local Similarity 45.5%; Pred. No. 1.6e-26;

Matches 61; Conservative 18; Mismatches 44; Indels 11; Gaps 2;

	Qy	38	KNMKVVFSQBELRKRLTPLQHVTQEKGTSAPEGEYTHHKDPGIIVKCVCVGTGPLFKSE	97
	Dd	15	KKM-----KEELNDMEYLVTQENGTEPPPFQNEYWNHFEGIYVDLKSGLPFTSE	64
	Qy	98	TTPDSGGWPSPHDVINSEAITFTDDPSYGMRHVETSCSQCAHLGHIIPDGPRPT-GKR	156
	Dd	65	DKFESNCGWPSFEKALNDEIVELVDKFCGMIRTVSRSEKANSHLGHFVNPDGPKEKGLR	124
	Qy	157	YCINSAALSFTPAD	170
	Dd	125	YCINSAAIOFIPOD	138

RESULT 11
US-08-361-083-212
; Sequence 212, Application US/08961083
; Patent No. 6159469
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigenes and Vaccines

Query Match	29.2%	Score 302.5;	DB 3;	Length 331;
Best Local Similarity	46.8%	Pred. No. 6.4e-26;		
Matches 59; Conservative 19; Mismatches 47; Indels 1; Gaps 1;				
Qy	46	SOQLRRLTPLQVHYVTOEKTESAFEGEYTHHKDPGLYKVCVCGTPLFKSETKFDSSG	105	
Db	196	SDEELKKTLSPEEYAVTQENQTERAFSNRYWDKFGESLYVDIAGEPLFSSKDKFESGCG	255	
Qy	106	WPSPHDVINSRAITFTDDFSYGMHVRVETSCSCQGAHLGHI FDDGPRPT -GRKYCINSAAL	164	
Db	256	WPSFTQISPDVVIYKEDKSYNMTMEVRSRVGDSHLGHVETDGPQDKGLRYCINSLSI	315	
Qy	165	SFTPAD	170	
Db	316	RFIPKD	321	

```

RESULT 12
US-09-536-784-212
; Sequence 212, Application US/09536784
; Patent No. 6573082
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/536,784
; FILING DATE: 30-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB340P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 212:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 331 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 212:
US-09-536-784-212

Query Match          29.2%   Score 302.5; DB 4; Length 331;
Best Local Similarity 46.8%; Pred. No. 6.4e-26;
Matches 59; Conservative 19; Mismatches 47; Indels 1; Gaps 1;

Qy    46 SQEELKRLPLQVHYVTQEKTSAFEGYTHHKDPGIYKCVGCTPLFKSETKFDSSGS 105
Db    196 SDEELKTLSPFEAYVTQENRATFAFNRYWDFESGIYYVDIATGEPLFSKKDKFESGCG 255

Qy    106 WPSFHVDVINSEATFTDDFSYGMRHVETSCSQCAHLGHIFDGPRTT-GKRYCINSAAL 164
Db    256 WPSFTQPISPDVVITYEDKSNNTRMEVRSGRVGDHSLGHVFTDGPQDGGLRLYCINLSI 315

Qy    165 SETPAD 170
Db    316 RFIKXD 321

RESULT 13
US-08-961-083-192
; Sequence 192, Application US/08961083
; Patent No. 6159469
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville

```

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OM protein - protein search, using sw model

Run on: September 3, 2005, 02:16:36 ; Search time 17 seconds
(without alignments)
1086.683 Million cell updates/sec

Title: US-10-245-013-48

Perfect score: 1036

Sequence: 1 MSPRTLPRPLSLCLSLC.....GTARGGSGVASPAQADKAEL 192

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

PIR 79:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	428.5	41.4	147	2 AP0711	conserved hypotet
2	423	40.8	202	2 H96576	hypothetical prote
3	407	39.3	151	2 A69195	transcription regu
4	406	39.2	132	2 A83293	conserved hypotet
5	405	39.1	137	1 B64938	hypothetical prote
6	405	39.1	137	2 G90939	hypothetical prote
7	405	39.1	137	2 C85788	hypothetical prote
8	396.5	38.3	137	2 AB0263	conserved hypotet
9	357	34.5	135	2 AD2688	transcription regu
10	357	34.5	135	2 G97469	hypothetical prote
11	351.5	33.9	147	2 D82131	PIB-related prote
12	349	33.7	133	2 H84294	transcription regu
13	344	33.2	143	2 G85830	hypothetical prote
14	342.5	33.1	145	2 B90575	hypothetical prote
15	342	33.0	164	2 AF2293	hypothetical prote
16	340	32.8	157	2 C75404	PIB-related prote
17	335	32.3	136	2 F70968	hypothetical prote
18	332.5	32.1	522	2 E82024	peptide methionine
19	332.5	32.1	522	2 G81243	peptide methionine
20	331.5	32.0	146	2 B97091	methionine sulfoxi
21	324.5	31.3	176	1 S74642	hypothetical prote
22	324	31.3	135	2 T35853	probable oxidoredu
23	323	31.2	394	2 C82439	peptide methionine
24	322	31.1	159	2 P87519	PIB-related prote
25	320.5	30.9	359	2 H64547	peptide methionine
26	318.5	30.7	147	2 B95392	protein imported
27	318.5	30.7	359	2 E71960	probable peptide m
28	314.5	30.4	143	2 F69940	transcription regu
29	313.5	30.3	353	2 E64124	peptide methionine

30	311	30.0	148	2	G82223	PIB-related prote
31	302.5	29.2	311	2	D95076	peptide methionine
32	302.5	29.2	370	2	A97944	peptide methionine
33	300	29.0	159	2	T44354	hypothetical prote
34	298	28.8	136	2	D85060	hypothetical prote
35	297.5	28.7	152	1	S44820	R44E2.6 protein -
36	293	28.3	146	2	AB3612	transcription regu
37	292	28.2	521	2	S02018	regulatory protein
38	291	28.1	151	1	S73506	PIB homolog K05.0
39	289.5	27.9	145	2	AC1307	transcription regu
40	287.5	27.8	142	2	G89919	conserved hypotet
41	286.5	27.7	145	2	AC1679	transcription regu
42	285.5	27.6	312	2	H95157	peptide methionine
43	285.5	27.6	312	2	H98033	peptide methionine
44	285	27.5	138	2	T39910	conserved hypotet
45	284.5	27.5	143	2	T05466	hypothetical prote
46	281.5	27.2	127	2	JC7624	hypothetical 14.2K
47	281.5	27.2	139	2	G85060	hypothetical prote
48	278.5	26.9	141	2	H85060	hypothetical prote
49	277.5	26.8	150	1	E64249	PIB repressor pi
50	276.5	26.7	155	2	D82755	conserved hypotet
51	274.5	26.5	141	2	T05465	hypothetical prote
52	273	26.4	142	2	E86648	reductase (impor
53	271	26.2	291	2	G71300	probable protein-m
54	263	25.4	168	1	S19361	hypothetical prote
55	255.5	24.7	224	2	S77828	probable transcrip
56	247.5	23.9	139	2	E85060	hypothetical prote
57	233	22.5	119	2	C81315	hypothetical prote
58	214	20.7	124	2	T05467	hypothetical prote
59	94	9.1	445	2	T33617	hypothetical prote
60	89	8.6	2895	2	T08437	hyperplastic discs
61	84.5	8.2	2194	1	JQ1977	glutamate synthase
62	82.5	8.0	710	2	T31502	hypothetical prote
63	79.5	7.7	1044	2	H69049	isoleucine-tRNA li
64	78.5	7.6	273	2	T01985	zinc-finger protei
65	78.5	7.6	322	2	T04535	hypothetical prote
66	77.5	7.5	358	2	F83875	hypothetical prote
67	77.5	7.5	1045	1	SYEXI	isoleucine-tRNA li
68	77	7.4	663	2	T03217	LIM domain protein
69	77	7.4	676	2	T01084	hypothetical prote
70	76	7.3	1184	1	A34795	kinesin-related pr
71	75.5	7.3	434	2	T01013	hypothetical prote
72	74.5	7.2	72	2	C86714	hypothetical prote
73	74.5	7.2	425	2	T48724	hypothetical prote
74	74.5	7.2	601	2	T34396	hypothetical prote
75	74	7.1	219	2	S16112	IG kappa chain V r
76	74	7.1	227	2	T39313	zinc-finger protei
77	74	7.1	239	2	S37923	cell wall protein
78	74	7.1	271	2	F64349	hypothetical prote
79	74	7.1	420	2	S65084	finger protein XFG
80	74	7.1	710	2	F86778	DNA topoisomerase
81	74	7.1	1712	2	A38261	masking protein pr
82	74	7.1	2344	1	R8WRH	genome polyprotein
83	74	7.1	2344	2	S64740	genome polyprotein
84	74	7.1	2344	2	S55399	genome polyprotein
85	74	7.1	3224	1	S58884	Ran-binding protei
86	73	7.0	193	2	S12658	cysteine-rich prot
87	73	7.0	493	2	A84443	probable ribonucle
88	73	7.0	532037	2	S32037	finger protein XFG
89	73	7.0	559	2	B55933	paxillin - chicken
90	73	7.0	1244	2	S25327	cytoskeleton assem
91	73	7.0	2399	2	H71879	hypothetical prote
92	72.5	7.0	474	2	S73677	toxin-like outer m
93	72.5	7.0	495	2	A83866	glutamate synthase
94	72.5	7.0	649	2	T32668	hypothetical prote
95	72.5	7.0	671	2	J80288	krueppel-type zinc
96	72.5	7.0	1115	1	IJMSNL	neural cell adhesi
97	72	6.9	176	2	A13362	peptidylprolyl iso
98	72	6.9	347	2	G70677	probable echa20 pr
99	72	6.9	333	2	T52594	squamosa promoter
100	72	6.9	339	2	S35068	hypothetical prote
101	72	6.9	346	2	C83172	hypothetical prote
102	72	6.9	400	2	E83675	hypothetical prote

103	72	6.9	422	2	T21820	hypothetical prote	176	68	6.6	624	2	T19630	hypothetical prote
104	71.5	6.9	145	2	G86191	hypothetical prote	177	68	6.6	675	2	S51037	zinc-finger protei
105	71.5	6.9	540	2	B57785	zinc finger protei	178	68	6.6	796	2	T23238	hypothetical prote
106	71.5	6.9	601	2	B36346	fibulin 1 precursor	179	68	6.6	1004	2	JC2221	major surface glyc
107	71.5	6.9	683	2	C36346	fibulin 1 precursor	180	68	6.6	1090	2	S59077	cellulose 1,4-beta
108	71.5	6.9	1042	2	AF0739	exodeoxyribonuclea	181	68	6.6	1199	2	JC4816	major surface glyc
109	71.5	6.9	1091	1	IJCHNL	neural cell adhesi	182	68	6.6	1299	2	T43251	furin (EC 3.4.21.7
110	71	6.9	195	2	H96586	hypothetical prote	183	68	6.6	1382	2	T23581	hypothetical prote
111	71	6.9	211	2	D85432	transcription fact	184	68	6.6	1840	2	T30250	GT1 protein - mous
112	71	6.9	337	2	I48691	regulatory protein	185	67.5	6.5	194	2	S52335	beta-cysteine-rich
113	71	6.9	387	2	JR0364	lactosylceramide a	186	67.5	6.5	194	2	S41761	cysteine-rich prot
114	71	6.9	413	2	AG2456	transposase all1520	187	67.5	6.5	414	2	S43253	alanine-glyoxylate
115	71	6.9	445	2	S32036	finger protein XFG	188	67.5	6.5	445	2	T51585	4-hydroxyphenylpr
116	71	6.9	462	2	I31699	gene XGF 5.1C prot	189	67.5	6.5	456	2	T19817	hypothetical prote
117	71	6.9	524	1	S36175	glycerol kinase (E	190	67.5	6.5	473	2	B86201	protein F12K11.9 [
118	71	6.9	979	2	T01566	hypothetical prote	191	67.5	6.5	594	2	JC5146	arylphorin gene-sp
119	71	6.9	1672	2	T46237	hypothetical prote	192	67.5	6.5	595	2	G02075	transcription repr
120	70.5	6.8	350	2	T48622	hypothetical prote	193	67.5	6.5	625	2	T20634	hypothetical prote
121	70.5	6.8	464	2	B55223	major tail protein	194	67.5	6.5	639	2	T43190	probable actin-bin
122	70.5	6.8	1468	2	A44345	nucleoporin - rat	195	67.5	6.5	650	2	G97100	DNA gyrase B chain
123	70	6.8	193	2	S53580	cysteine-rich prot	196	67.5	6.5	732	2	S47073	finger protein HZF
124	70	6.8	294	2	T08408	transcription fact	197	67.5	6.5	739	2	A26016	lysine decarboxyla
125	70	6.8	356	2	A25918	thrombomodulin - b	198	67.5	6.5	761	1	S52769	subtilisin-like pr
126	70	6.8	389	2	T71097	hypothetical prote	199	67.5	6.5	882	2	H97479	aminopeptidase N (
127	70	6.8	402	1	TVEFVR	protein-tyrosine k	200	67.5	6.5	882	2	AH2697	aminopeptidase N p
128	70	6.8	468	2	A29650	wingless (wg) prot	201	67.5	6.5	1641	2	T10955	early nodulin bind
129	70	6.8	469	1	TVEFTR	transforming prote	202	67.5	6.5	2077	1	WZBR24	240K tegument prot
130	70	6.8	582	2	S08686	finger protein ZFP	203	67.5	6.5	2647	2	A37098	gelation factor AB
131	70	6.8	922	1	S54342	protein-tyrosine-p	204	67	6.5	229	2	A48927	Kruppel-like zinc
132	70	6.8	976	2	D96714	DNA-directed RNA p	205	67	6.5	264	2	F71272	probable peptidyl-
133	70	6.8	1009	2	T32464	hypothetical prote	206	67	6.5	297	2	G69892	UTP-glucose-1-phos
134	69.5	6.7	200	2	G93307	polyferredoxin (mv	207	67	6.5	411	2	T15705	hypothetical prote
135	69.5	6.7	310	2	A41776	syndecan 1 precurs	208	67	6.5	421	2	A60058	neural cell adhesi
136	69.5	6.7	374	1	F70584	phosphate specific	209	67	6.5	451	2	A45643	tubulin alpha chai
137	69.5	6.7	661	1	OXRTA2	acyl-CoA oxidase (210	67	6.5	495	2	S76280	amphiphosphoribosy
138	69.5	6.7	1042	2	T26644	hypothetical prote	211	67	6.5	706	2	A48752	B-cell CLL/lymphom
139	69.5	6.7	1103	2	T04617	hypothetical prote	212	67	6.5	706	2	I52586	B-cell CLL/lymphom
140	69.5	6.7	1670	1	CSHUB	collagen alpha 3(I	213	67	6.5	825	2	S55060	feritin alpha-II
141	69.5	6.7	1693	2	T30867	Rho-guanine nucleo	214	67	6.5	956	2	G70327	isoleucine-tRNA li
142	69	6.7	149	2	T25858	hypothetical prote	215	67	6.5	1012	2	T41940	DNA polymerase - h
143	69	6.7	258	2	S57960	CABP protein beta	216	67	6.5	1017	2	S67804	LRG1 protein - yea
144	69	6.7	308	2	T46026	hypothetical prote	217	67	6.5	1047	2	D71302	probable exonuclea
145	69	6.7	348	2	I38599	zinc finger protei	218	67	6.5	1219	2	T14578	nucleoporin Nup153
146	69	6.7	401	2	A42177	KRAB-domain-contai	219	67	6.5	1251	2	A57293	latent transformatin
147	69	6.7	615	2	AH2248	proteinase (import	220	67	6.5	1548	2	S34583	serine proteinase
148	69	6.7	778	2	A60798	platelet glycoprot	221	67	6.5	2409	1	A60379	versican precursor
149	69	6.7	778	2	A60798	platelet glycoprot	222	67	6.5	2611	2	T14591	actinomycin synthe
150	69	6.7	788	2	A26547	platelet glycoprot	223	66.5	6.4	340	2	G70741	hypothetical prote
151	69	6.7	788	2	A26547	platelet glycoprot	224	66.5	6.4	405	2	C72305	transposase, IS605
152	69	6.7	1026	2	T19631	protein-tyrosine-p	225	66.5	6.4	437	2	B53193	hedghog homolog v
153	68.5	6.6	135	1	W6WLEP	E6 protein - Europ	226	66.5	6.4	471	2	T20690	hypothetical prote
154	68.5	6.6	192	2	A49648	cysteine-rich prot	227	66.5	6.4	491	2	S51435	hypothetical prote
155	68.5	6.6	192	2	S38879	LIM-domain protein	228	66.5	6.4	701	2	T14757	hypothetical prote
156	68.5	6.6	211	2	T34616	NADH2 dehydrogenas	229	66.5	6.4	715	2	B90418	DNA helicase relat
157	68.5	6.6	273	2	H75393	conserved hypotet	230	66.5	6.4	1027	2	I38604	p53-binding protei
158	68.5	6.6	295	2	D84902	probable WRKY-type	231	66.5	6.4	1108	2	A48508	cyclic-nucleotide
159	68.5	6.6	373	2	AH1752	protein gp20 (Bact	232	66.5	6.4	1445	2	T10728	probable gas/pol p
160	68.5	6.6	528	2	T41362	hypothetical prote	233	66.5	6.4	1820	2	A55494	latent transformatin
161	68.5	6.6	620	2	I38095	acyl-CoA oxidase (234	66.5	6.4	2077	2	T44178	large tegument pro
162	68.5	6.6	893	2	H96651	protein T3P18.19 [235	66.5	6.4	6260	2	T30228	polyketide synthas
163	68.5	6.6	1597	1	BVEPFI	sol protein, large	236	66	6.4	136	2	F69041	transcription elon
164	68.5	6.6	1597	2	T08428	gene small optic l	237	66	6.4	194	2	A55099	muscle LIM protein
165	68.5	6.6	2871	2	A55567	fibrillin I - bovi	238	66	6.4	265	2	E95926	hypothetical membr
166	68	6.6	194	2	S57472	murine muscle LIM	239	66	6.4	460	2	T40799	endo-1,4-beta-gluc
167	68	6.6	302	2	H65113	hypothetical 30.8	240	66	6.4	528	2	T22941	hypothetical prote
168	68	6.6	341	2	C69789	hypothetical prote	241	66	6.4	763	2	D86326	hypothetical prote
169	68	6.6	355	2	A127541	hypothetical prote	242	66	6.4	805	2	H72098	DNA gyrase, chain
170	68	6.6	510	2	T37541	probable glycolipi	243	66	6.4	805	2	C86525	DNA gyrase subunit
171	68	6.6	513	2	T44290	biotin carboxylase	244	66	6.4	1008	2	T05578	hypothetical prote
172	68	6.6	522	2	E84833	hypothetical prote	245	66	6.4	1186	2	T33754	O/E-1-associated z
173	68	6.6	524	2	JN0606	ATP-stimulated glu	246	66	6.4	1396	1	VCB840	major capsid prote
174	68	6.6	557	2	A55933	paxillin - human	247	66	6.4	1979	2	JW0059	metpr protein - mo
175	68	6.6	610	2	T06280	probable starch sy	248	66	6.4	2447	2	T16870	hypothetical prote

249 66 6.4 3005 2 S33642 homeotic protein z
 250 66 6.4 3106 1 S53868 laminin alpha-2 ch
 251 65.5 6.3 122 2 S40338 Ig kappa chain - h
 252 65.5 6.3 218 2 S43016 adenylate kinase (h
 253 65.5 6.3 298 2 G75140 hypothetical prote
 254 65.5 6.3 301 1 Z3BP13 gene 301 protein -
 255 65.5 6.3 401 2 T16706 hypothetical prote
 256 65.5 6.3 506 2 S37583 RING finger protei
 257 65.5 6.3 513 1 TVHURF ret finger protein
 258 65.5 6.3 605 2 S18648 protein kinase wis
 259 65.5 6.3 662 2 T32821 hypothetical prote
 260 65.5 6.3 677 2 J7C7303 pectate lyase (EC
 261 65.5 6.3 685 2 S78040 fibulin, splice fo
 262 65.5 6.3 705 2 S34968 fibulin, splice fo
 263 65.5 6.3 794 2 S59069 Z13 protein - mous
 264 65.5 6.3 801 4 TVHURE transforming prote
 265 65.5 6.3 1002 2 T19226 hypothetical prote
 266 65.5 6.3 1028 2 C88364 protein C13B4.1 [i
 267 65.5 6.3 1378 2 T30173 zinc finger protei
 268 65.5 6.3 1417 2 H30670 probable invasiv
 269 65.5 6.3 1417 2 D85521 probable adhesin
 270 65.5 6.3 1466 2 T39557 vacuolar protein
 271 65.5 6.3 1571 2 T14155 zinc finger protei
 272 65.5 6.3 1983 2 T00385 KIAA0624 protein -
 273 65.5 6.3 3002 2 A47221 fibrillin 1 precu
 274 65.5 6.3 3672 2 T23433 hypothetical prote
 275 65.5 6.3 3704 2 T37316 probable laminin
 276 65 6.3 122 2 S19396 probable membrane
 277 65 6.3 182 2 B84387 hypothetical prote
 278 65 6.3 201 2 AC0255 probable phage pro
 279 65 6.3 215 2 T45846 zinc-finger-like p
 280 65 6.3 301 2 AP2223 heterodisulfide re
 281 65 6.3 323 2 F84185 transcripition in
 282 65 6.3 430 1 CMUMF mucorpepsin (EC 3.
 283 65 6.3 459 2 T16632 hypothetical prote
 284 65 6.3 548 2 T46565 tRNA (guanine-N2-)
 285 65 6.3 644 2 A36325 epidermal growth f
 286 65 6.3 661 2 T48943 hypothetical prote
 287 65 6.3 705 2 S55420 conserved hypothet
 288 65 6.3 803 2 S26823 zinc finger protei
 289 65 6.3 817 2 S33793 hypothetical prote
 290 65 6.3 851 2 AF00118 penicillin-binding
 291 65 6.3 1184 2 A55184 fibulin-2 precursor
 292 65 6.3 1265 2 S57968 Ran-binding protei
 293 65 6.3 1701 2 T43213 ENBP1 protein - ba
 294 65 6.3 4845 2 T31067 BIR repeat contain
 295 64.5 6.2 101 2 T50836 Yippee protein (im
 296 64.5 6.2 164 2 S06779 zinc finger protei
 297 64.5 6.2 283 2 T27423 hypothetical prote
 298 64.5 6.2 352 2 S16547 neutral proteinase
 299 64.5 6.2 360 2 B35411 alkalal monooxygen
 300 64.5 6.2 379 1 T03448 dihydrokaempferol
 301 64.5 6.2 396 2 B69325 LPS biosynthesis p
 302 64.5 6.2 449 1 LIPG triacylglycerol li
 303 64.5 6.2 572 2 S19311 Kruppel-type zinc
 304 64.5 6.2 737 1 S28942 protein kinase C (h
 305 64.5 6.2 816 2 S05548 gap protein bunchb
 306 64.5 6.2 1106 2 T13938 gene shuttle craft
 307 64.5 6.2 1456 2 T10397 LTR gag/pol polypr
 308 64.5 6.2 1732 2 T14039 protein kinase (EC
 309 64.5 6.2 2924 2 T18378 variant-specific s
 310 64.5 6.2 3418 1 G02334 breast cancer tumo
 311 64 6.2 200 2 T16264 hypothetical prote
 312 64 6.2 201 2 A39486 gamma-hemolysin co
 313 64 6.2 286 2 C49238 lectin precursor -
 314 64 6.2 290 2 JX0175 probable N-acetyl
 315 64 6.2 302 2 G91140 probable NAGC-like
 316 64 6.2 302 2 B85986 leucocidin R S com
 317 64 6.2 315 2 A49234 leucocidin chain S
 318 64 6.2 315 2 JN0626 leucocidin chain co
 319 64 6.2 315 2 E90043 gamma-hemolysin co
 320 64 6.2 315 2 PC4078 hlgC-like protein
 321 64 6.2 326 2 T52407 RING-H2 zinc finge

322 64 6.2 344 2 I45894
 323 64 6.2 425 1 A26431
 324 64 6.2 427 2 T04869 nerve growth facto
 325 64 6.2 495 2 B87869 transforming prote
 326 64 6.2 513 2 A96842 F23A5.27 [imported
 327 64 6.2 529 2 I39658 E23A5.27 [imported
 328 64 6.2 566 2 T24696 isoleucine-tRNA li
 329 64 6.2 574 2 A46054 hypothetical prote
 330 64 6.2 600 2 T02266 GTP-binding protei
 331 64 6.2 613 2 JC7992 negatively regulat
 332 64 6.2 699 2 P95146 DNA topoisomerase
 333 64 6.2 700 2 S12335 DEAD box protein -
 334 64 6.2 701 2 D98014 DNA topoisomerase
 335 64 6.2 822 2 B49151 fibroblast growth
 336 64 6.2 862 2 I49583 differentiation an
 337 64 6.2 865 2 T34584 probable secreted
 338 64 6.2 876 2 AH1964 acornate hydratae
 339 64 6.2 890 2 T30103 hypothetical prote
 340 64 6.2 969 2 AB3388 soluble lytic mure
 341 64 6.2 1011 2 T51399 DNA-directed RNA p
 342 64 6.2 1077 2 A44067 serine-rich protei
 343 64 6.2 1099 2 T14850 S-layer protein pr
 344 64 6.2 1584 2 T22674 hypothetical prote
 345 64 6.2 1817 2 T10689 hypothetical prote
 346 64 6.2 2471 2 A49128 cell-fate determin
 347 63.5 6.1 98 1 BORT2 prostatic steroid-
 348 63.5 6.1 267 2 H86548 polymorphic outer
 349 63.5 6.1 277 2 B80843 probable protopor
 350 63.5 6.1 277 2 B85701 probable protopor
 351 63.5 6.1 326 2 B82343 ROK family protein
 352 63.5 6.1 329 2 A61155 isopenicillin N sy
 353 63.5 6.1 329 2 T20546 hypothetical prote
 354 63.5 6.1 380 2 I50701 transcription fact
 355 63.5 6.1 394 2 T24860 hypothetical prote
 356 63.5 6.1 437 2 A49425 Sonic hedgehog pro
 357 63.5 6.1 475 2 S03679 finger protein (cl
 358 63.5 6.1 478 2 T51274 hypothetical prote
 359 63.5 6.1 517 2 T25615 hypothetical prote
 360 63.5 6.1 557 2 T16815 hypothetical prote
 361 63.5 6.1 562 2 T42250 polypeptide N-acet
 362 63.5 6.1 603 2 S51461 polypeptide N-acet
 363 63.5 6.1 617 2 T42249 polypeptide N-acet
 364 63.5 6.1 618 2 T42248 tetracycline resis
 365 63.5 6.1 639 1 A48900 trophozoite cystei
 366 63.5 6.1 677 2 C42125 hypothetical prote
 367 63.5 6.1 757 2 T42693 hypothetical prote
 368 63.5 6.1 1106 2 T44598 zinc finger protei
 369 63.5 6.1 1167 2 T34020 enamein matrix pr
 370 63.5 6.1 1274 2 T37193 antigen containing
 371 63.5 6.1 1567 2 T03730 hypothetical prote
 372 63.5 6.1 1956 2 T00051 probable rubB prot
 373 63 6.1 60 2 D70593 hypothetical prote
 374 63 6.1 180 2 S28716 superoxide dismuta
 375 63 6.1 195 2 S00157 Ig kappa chain pre
 376 63 6.1 225 2 J10029 RING-H2 finger pro
 377 63 6.1 273 2 T51855 bone marrow stroma
 378 63 6.1 318 2 I59301 delta-aminolevulin
 379 63 6.1 323 2 C64540 hypothetical prote
 380 63 6.1 334 2 T22215 RING-H2 zinc finge
 381 63 6.1 334 2 T49217 glutamyl endopepti
 382 63 6.1 357 1 S33321 probable hydro-ly
 383 63 6.1 365 1 S06725 subtilisin (EC 3.4
 384 63 6.1 382 1 SUBSN finger protein odd
 385 63 6.1 392 2 S11998 flagellin modifia
 386 63 6.1 402 2 A87278 two-component sens
 387 63 6.1 469 2 E75423 aldehyde dehydroge
 388 63 6.1 470 2 H64906 hypothetical prote
 389 63 6.1 510 2 E30418 probable membrane
 390 63 6.1 524 2 S55097 sterol 27-monooxyg
 391 63 6.1 531 1 A39740 hypothetical prote
 392 63 6.1 537 2 A86154 hypothetical prote
 393 63 6.1 538 2 T49418 subunit F of alkyl
 394 63 6.1 571 2 H82668

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 finger protein odd
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 probable membrane
 sterol 27-monooxyg
 hypothetical prote
 hypothetical prote
 subunit F of alkyl

395	63	6.1	700	2	B41897	cellulase (EC 3.2.	468	62	6.0	263	2	T39487	hypothetical prote
396	63	6.1	717	2	H72208	conserved hypothet	469	62	6.0	275	2	B69648	5-keto-4-deoxyuron
397	63	6.1	736	1	KIRBCE	protein kinase C (470	62	6.0	277	1	MPHUP	myelin proteolipid
398	63	6.1	737	1	KIMSC	protein kinase C (471	62	6.0	277	1	MPHUP	myelin proteolipid
399	63	6.1	737	1	KIRTC	protein kinase C (472	62	6.0	277	1	S43792	myelin proteolipid
400	63	6.1	769	2	F85077	probable transposo	473	62	6.0	277	1	A43548	myelin proteolipid
401	63	6.1	819	1	TNBE11	91.8K alpha trans-	474	62	6.0	291	2	S05508	photosystem II oxy
402	63	6.1	888	2	D84824	probable DNA-dirc	475	62	6.0	314	2	T30921	hypothetical prote
403	63	6.1	910	2	C81832	transferrin-bindin	476	62	6.0	335	2	A75179	probable proteinase
404	63	6.1	1073	2	B36429	integrin alpha-6 c	477	62	6.0	398	2	D84212	threonine phosphat
405	63	6.1	1079	2	I59362	calcium/polyvalent	478	62	6.0	443	2	C89863	glucose-6-phosphat
406	63	6.1	1080	2	G81739	transcription-repa	479	62	6.0	445	2	T23199	hypothetical prote
407	63	6.1	1091	2	A41543	integrin alpha-6 c	480	62	6.0	450	2	JQ1614	gastin receptor -
408	63	6.1	1152	2	AC1347	probable peptidogl	481	62	6.0	460	2	JC1299	endo-beta-1,4-gluc
409	63	6.1	1227	2	A86245	hypothetical protei	482	62	6.0	482	2	T02538	hypothetical prote
410	63	6.1	1776	1	RWPYH	genome polyprotein	483	62	6.0	501	2	I46701	cholesterol 7alpha
411	63	6.1	2124	2	A28452	proteoglycan core	484	62	6.0	515	2	T09203	probable tail comp
412	63	6.1	2145	2	S61041	glutamate synthase	485	62	6.0	515	2	T09272	probable tail comp
413	63	6.1	2356	2	T27790	hypothetical prote	486	62	6.0	520	2	T30808	hypothetical prote
414	63	6.1	4351	2	T00252	MEGF1 protein - ra	487	62	6.0	524	2	G86834	alpha-amylase (EC
415	63	6.1	4545	1	S25111	alpha-2-macroglobu	488	62	6.0	530	2	JH0167	potassium channel
416	62.5	6.0	114	2	S49572	Ig kappa chain pre	489	62	6.0	550	2	I64203	aspartate-tRNA lig
417	62.5	6.0	148	2	T23839	hypothetical prote	490	62	6.0	555	2	T21028	hypothetical prote
418	62.5	6.0	182	2	AC0545	hypothetical prote	491	62	6.0	637	2	I49638	probable RNA helic
419	62.5	6.0	213	2	T34949	hypothetical prote	492	62	6.0	675	2	T35959	methylnalonyl-CoA
420	62.5	6.0	224	2	S17479	DCU protein precu	493	62	6.0	676	2	P85107	hypothetical prote
421	62.5	6.0	251	2	D86822	hypothetical prote	494	62	6.0	700	2	S23052	long-chain-fatty-a
422	62.5	6.0	252	2	S06567	finger protein (cl	495	62	6.0	705	2	T04052	hypothetical prote
423	62.5	6.0	256	2	E88469	protein C2H8.6 [i	496	62	6.0	735	2	I48101	ADAM 6 protein pre
424	62.5	6.0	259	2	G81833	hypothetical prote	497	62	6.0	911	2	JN0821	transferrin-bindin
425	62.5	6.0	264	2	AC3302	7alpha-hydroxyter	498	62	6.0	915	2	A43335	transferrin-bindin
426	62.5	6.0	264	2	A84245	hypothetical prote	499	62	6.0	915	2	P81196	transferrin-bindin
427	62.5	6.0	269	2	T37418	probable 30.8K pro	500	62	6.0	925	1	A39216	nucleotide diphosp
428	62.5	6.0	277	2	T07637	hypothetical prote	501	62	6.0	1339	2	JC4387	epidermal growth f
429	62.5	6.0	294	2	E81420	probable flagellar	502	62	6.0	1553	2	T03301	rab3 effector prot
430	62.5	6.0	338	2	T18715	hypothetical prote	503	62	6.0	1829	2	T14280	RM1 protein - mous
431	62.5	6.0	342	2	T46909	hypothetical prote	504	62	6.0	1832	2	T31113	mucin-like glycopr
432	62.5	6.0	344	2	A32141	foliistatin 1 prec	505	61.5	5.9	106	2	S28239	NADH2 dehydrogenas
433	62.5	6.0	344	2	A83298	hypothetical prote	506	61.5	5.9	131	2	A31676	brain natriuretic
434	62.5	6.0	373	2	S06010	finger protein ego	507	61.5	5.9	131	2	A33873	brain natriuretic
435	62.5	6.0	384	2	S36529	E2 protein - human	508	61.5	5.9	133	2	S42611	conserved hypothet
436	62.5	6.0	395	2	B75047	probable 2-oxoliov	509	61.5	5.9	147	2	AC1367	zinc finger protei
437	62.5	6.0	395	2	A46031	immobilization sur	510	61.5	5.9	195	2	S00754	hypothetical prote
438	62.5	6.0	399	2	T00631	hypothetical prote	511	61.5	5.9	235	2	A81174	hypothetical prote
439	62.5	6.0	416	1	JN0006	nerve growth facto	512	61.5	5.9	270	2	JQ1768	SalL2L protein - v
440	62.5	6.0	433	2	S62201	formylmethanofuran	513	61.5	5.9	270	2	T28577	7L protein - vario
441	62.5	6.0	441	2	T25193	hypothetical prote	514	61.5	5.9	270	2	I36851	ATP/GTP-binding pr
442	62.5	6.0	500	2	A48767	glutamate decarbox	515	61.5	5.9	270	2	A72168	A36L protein - var
443	62.5	6.0	531	2	G89657	protein F1785.2 [i	516	61.5	5.9	290	2	AE1949	hypothetical prote
444	62.5	6.0	553	2	I37417	glycerol kinase -	517	61.5	5.9	300	2	G42520	A32L protein - vac
445	62.5	6.0	574	2	A37197	estrogen receptor	518	61.5	5.9	305	2	B84779	hypothetical prote
446	62.5	6.0	581	2	F84599	probable kinesin h	519	61.5	5.9	307	2	T51865	M55-like protein [
447	62.5	6.0	587	2	T21074	hypothetical prote	520	61.5	5.9	324	2	JC2395	Pas antigen precu
448	62.5	6.0	681	2	T39950	cell cycle inhibit	521	61.5	5.9	335	2	D81724	hypothetical prote
449	62.5	6.0	705	2	S34271	ribonucleoside-dip	522	61.5	5.9	343	2	T20073	hypothetical prote
450	62.5	6.0	745	2	G72453	hypothetical prote	523	61.5	5.9	344	2	I57698	foliistatin - rat
451	62.5	6.0	844	2	C86339	protein F2D10.12 [524	61.5	5.9	385	2	D87723	protein R06A10.2 [
452	62.5	6.0	913	2	S20590	exo-alpha-sialidas	525	61.5	5.9	385	2	A75317	hypothetical prote
453	62.5	6.0	1369	2	T43433	alpha-glucan synth	526	61.5	5.9	410	2	A40505	early protein BP0
454	62.5	6.0	1407	2	B72078	polymorphic outer	527	61.5	5.9	411	1	HYSNFA	ATP-dependent clp
455	62.5	6.0	1797	2	T21889	hypothetical prote	528	61.5	5.9	423	2	AD0558	probable flavoprot
456	62.5	6.0	1805	2	T21888	hypothetical prote	529	61.5	5.9	479	2	AD0845	finger protein HZF
457	62.5	6.0	2301	1	GNNTN	genome polyprotein	530	61.5	5.9	488	2	S47072	cell fusion glycop
458	62.5	6.0	2303	1	GNNTN	genome polyprotein	531	61.5	5.9	537	1	JQ1619	interleukin-1 [i
459	62.5	6.0	2303	2	S13554	genome polyprotein	532	61.5	5.9	558	2	B88500	protein R0467.1 [i
460	62.5	6.0	2464	1	ORMSP1	microtubule-associ	533	61.5	5.9	562	2	G02426	interleukin-1 rece
461	62.5	6.0	2871	2	A55624	fibrillin-1 precu	534	61.5	5.9	575	1	QOVZHS	H5 protein - vacci
462	62.5	6.0	4152	2	T31102	filamentous hemagg	535	61.5	5.9	646	2	H96565	protein F22C12.10
463	62.5	6.0	4919	2	T31105	hypothetical prote	536	61.5	5.9	655	1	A46888	hepatocyte growth
464	62.5	6.0	109	2	T02762	anther specific pr	537	61.5	5.9	660	1	B54942	acyl-CoA oxidase (
465	62	6.0	212	2	B86561	glycerol-3-P acylt	538	61.5	5.9	728	2	S21913	BKcore-TNfr1-Qi-21
466	62	6.0	212	2	B72063	probable 1-acylgly	539	61.5	5.9	783	2	T35389	probable serine-th
467	62	6.0	237	2	A83541	hypothetical prote	540	61.5	5.9	792	2	A71822	hypothetical prote

541	61.5	5.9	795	1	QOVZ44	H4L protein - vacc	614	61	5.9	843	2	A27131	epidermal growth f
542	61.5	5.9	795	2	T37370	RAP 94 - vaccinia	615	61	5.9	905	2	S55059	fertilin alpha-I -
543	61.5	5.9	979	1	J23349	protein-tyrosine-p	616	61	5.9	1051	2	A39712	kinase-like protei
544	61.5	5.9	995	2	AB1398	formate dehydrogen	617	61	5.9	1052	2	H83909	cell wall-associat
545	61.5	5.9	995	2	AE1773	formate dehydrogen	618	61	5.9	1123	2	T51517	telomerase reverse
546	61.5	5.9	996	1	S06635	Na+/K+-exchanging	619	61	5.9	1174	2	T08196	hypothetical prote
547	61.5	5.9	996	2	I48721	PTP 35 protein - m	620	61	5.9	1338	2	S09882	protein-tyrosine k
548	61.5	5.9	1042	2	T16169	hypothetical prote	621	61	5.9	1355	2	S40022	spalt protein - fr
549	61.5	5.9	1079	2	E87689	hypothetical prote	622	61	5.9	1388	2	T34157	hypothetical prote
550	61.5	5.9	1170	2	A40558	thrombospondin 1 p	623	61	5.9	2195	2	T34264	pyrimidine synthe
551	61.5	5.9	1188	2	T46608	zinc finger protei	624	61	5.9	2214	1	QZBYU2	kinase-related pro
552	61.5	5.9	1287	2	T44051	hypothetical prote	625	61	5.9	2311	1	TVCNHR	fibrillin-2 precu
553	61.5	5.9	1287	2	T42658	hypothetical prote	626	61	5.9	2918	2	A54105	hypothetical prote
554	61.5	5.9	1331	2	A48954	mannan endo-1,4-be	627	61	5.9	3375	2	T19821	LDL-receptor-relat
555	61.5	5.9	1350	2	S00647	finger protein - A	628	61	5.9	4753	1	A47437	probable metal-bin
556	61.5	5.9	1531	2	T42218	slit-1 protein hom	629	60.5	5.8	80	2	G96953	hypothetical prote
557	61.5	5.9	2206	1	GNNY2W	genome polyprotein	630	60.5	5.8	139	2	E71036	r40g3 protein - ri
558	61.5	5.9	2206	1	GNNY4P	genome polyprotein	631	60.5	5.8	204	2	T03962	probable hydrolase
559	61.5	5.9	2206	1	GNNY21	genome polyprotein	632	60.5	5.8	230	2	F83273	chitinase class IV
560	61.5	5.9	2206	1	GNNY27	genome polyprotein	633	60.5	5.8	266	2	S65778	isopenicillin N sy
561	61.5	5.9	2206	2	S03822	genome polyprotein	634	60.5	5.8	329	2	A29894	finger protein (cl
562	61.5	5.9	2207	1	GNNY1P	genome polyprotein	635	60.5	5.8	336	2	S06573	acetylsermidine d
563	61.5	5.9	2207	1	GNNY5P	genome polyprotein	636	60.5	5.8	337	2	AB3440	hypothetical prote
564	61.5	5.9	2207	2	S09553	genome polyprotein	637	60.5	5.8	340	2	T34762	hypothetical prote
565	61.5	5.9	2209	1	GNNY2P	genome polyprotein	638	60.5	5.8	359	2	A46509	B cell differentia
566	61.5	5.9	2214	1	A48548	genome polyprotein	639	60.5	5.8	392	2	S72436	RNA-binding hypothet
567	61.5	5.9	2899	2	T21546	hypothetical prote	640	60.5	5.8	393	2	AE3164	conserved hypothet
568	61.5	5.9	2915	2	G87867	hypothetical prote	641	60.5	5.8	407	2	D96721	hypothetical prote
569	61.5	5.9	13055	2	T16580	hypothetical prote	642	60.5	5.8	411	2	F91074	probable flavodoxi
570	61	5.9	77	2	G02666	cysteine-rich prot	643	60.5	5.8	411	2	E85919	probable flavodoxi
571	61	5.9	99	2	D86931	hypothetical prote	644	60.5	5.8	420	2	T47998	hypothetical prote
572	61	5.9	102	2	T49479	hypothetical prote	645	60.5	5.8	424	2	A48709	hypothetical prote
573	61	5.9	120	2	T45451	hypothetical prote	646	60.5	5.8	424	2	D90690	ATP-dependent clip
574	61	5.9	143	2	A87706	hypothetical prote	647	60.5	5.8	424	2	H85540	ATP-dependent clip
575	61	5.9	154	2	A64097	hypothetical prote	648	60.5	5.8	431	2	F71476	probable sodium-tr
576	61	5.9	187	2	T18844	hypothetical prote	649	60.5	5.8	431	2	I59572	Ikaro DNA binding
577	61	5.9	197	2	F82029	probable periplasm	650	60.5	5.8	432	2	T00949	hypothetical prote
578	61	5.9	201	1	VAPT	plasma retinol-bin	651	60.5	5.8	439	2	D97751	histidine-tRNA lig
579	61	5.9	210	2	B81008	hypothetical prote	652	60.5	5.8	441	2	T13000	hypothetical prote
580	61	5.9	211	2	B84035	hypothetical prote	653	60.5	5.8	460	2	A12264	aldehyde dehydroge
581	61	5.9	213	2	T14945	hypothetical prote	654	60.5	5.8	461	2	T01825	hypothetical prote
582	61	5.9	252	2	T03873	photosystem II oxy	655	60.5	5.8	471	2	P80154	125K surface anti
583	61	5.9	270	2	T29408	hypothetical prote	656	60.5	5.8	479	1	B65051	serine/threonine k
584	61	5.9	273	2	S69193	probable finger pr	657	60.5	5.8	480	2	T47255	seryl-tRNA synthet
585	61	5.9	274	2	T48086	hypothetical prote	658	60.5	5.8	482	2	B87497	cytochrome P450 2F
586	61	5.9	280	2	T19363	hypothetical prote	659	60.5	5.8	491	2	A56036	glutamate decarbox
587	61	5.9	283	2	C64379	hypothetical prote	660	60.5	5.8	496	2	T01962	DNA-binding protei
588	61	5.9	295	2	T04483	probable ring fing	661	60.5	5.8	518	2	A56355	acetate-CoA ligase
589	61	5.9	305	2	E84848	probable RING zinc	662	60.5	5.8	527	2	A84050	probable proteinas
590	61	5.9	343	2	S45321	follistatin - mous	663	60.5	5.8	543	2	T35352	hypothetical prote
591	61	5.9	344	1	A27701	probable GDSL-moti	664	60.5	5.8	547	2	T34318	asparagine synthe
592	61	5.9	358	2	T00578	alkanal monooxygen	665	60.5	5.8	563	2	D82846	flageelin - bacter
593	61	5.9	360	2	C42951	GTP-binding regula	666	60.5	5.8	565	2	I41061	integrin beta-6 ch
594	61	5.9	375	2	T37245	tail fiber protein	667	60.5	5.8	577	2	B37057	integrin beta-6 ch
595	61	5.9	382	2	S13237	protein phosphatas	668	60.5	5.8	598	2	T47254	probable protein k
596	61	5.9	414	2	S62462	polysialacturonase	669	60.5	5.8	620	2	S22711	translational elon
597	61	5.9	460	2	T17011	sensor kinase phoQ	670	60.5	5.8	693	2	E30579	hypothetical prote
598	61	5.9	487	1	VZEBPT	sensor kinase phoQ	671	60.5	5.8	711	2	AG0841	ribonucleoside-dip
599	61	5.9	487	2	AG0646	interleukin-9 rece	672	60.5	5.8	714	2	AG0841	hypothetical prote
600	61	5.9	522	2	B45268	N2,N2-dimethylguan	673	60.5	5.8	735	2	B69139	probable type III
601	61	5.9	524	2	T39993	scd2 protein - fla	674	60.5	5.8	779	2	E71825	gelsolin precursor
602	61	5.9	536	2	T38210	hypothetical prote	675	60.5	5.8	832	1	FAHUP	hypothetical prote
603	61	5.9	571	2	B84585	epithelial sodium	676	60.5	5.8	858	2	T31792	penicillin-binding
604	61	5.9	640	2	I51915	topoisomerase I XF	677	60.5	5.8	1003	2	C84601	hypothetical prote
605	61	5.9	660	2	C82861	hypothetical prote	678	60.5	5.8	1048	2	T30815	platelet-derived g
606	61	5.9	680	2	E72033	hypothetical prote	680	60.5	5.8	1072	2	A38457	integrin alpha-6 c
607	61	5.9	686	2	B86590	hypothetical prote	681	60.5	5.8	1130	2	T17399	probable DEAH ATP-
608	61	5.9	686	2	A34612	zinc finger protei	682	60.5	5.8	1274	2	T42017	cysteine rich prot
609	61	5.9	687	2	A49636	soluble vascular e	683	60.5	5.8	1311	2	T33757	hypothetical prote
610	61	5.9	719	2	T30438	exoglucanase - Clo	684	60.5	5.8	1702	2	T14050	protein kinase (BC
611	61	5.9	743	2	T09173	BH domain protein	685	60.5	5.8	1826	2	H86502	excinuclease ABC s
612	61	5.9	769	2	I56546	Shaw type potassiu	686	60.5	5.8				
613	61	5.9	822	2	S19947	fibroblast growth							

687	60.5	5.8	1826	2	D72120	excinuclease ABC,	760	60	5.8	1222	2	S40977	hypothetical prote
688	60.5	5.8	1891	2	T13594	hypothetical prote	761	60	5.8	1767	2	T00458	hypothetical prote
689	60.5	5.8	2078	2	T09326	tegment protein -	762	60	5.8	1808	2	T15099	hypothetical prote
690	60.5	5.8	2194	1	GNNYE7	genome polyprotein	763	60	5.8	1998	2	T13009	hypothetical prote
691	60.5	5.8	2334	2	S32920	cell wall-associat	764	60	5.8	2282	2	T42717	DNA-binding protei
692	60.5	5.8	2395	1	S50820	surface protein ty	765	60	5.8	3623	2	T09456	intrinsic factor-B
693	60.5	5.8	2508	2	S61441	surface-associated	766	59.5	5.7	76	2	E64453	hypothetical prote
694	60.5	5.8	2756	2	T30183	hypothetical prote	767	59.5	5.7	105	2	T45087	pyruvate synthase
695	60.5	5.8	2802	2	F97686	hypothetical prote	768	59.5	5.7	162	2	B72547	probable aspartate
696	60.5	5.8	2831	2	F97686	cyclic beta-(1-2)	769	59.5	5.7	174	2	F87251	isoquinoline 1-oxi
697	60.5	5.8	3036	2	A12911	beta (1->2) glucan	770	59.5	5.7	181	2	E97341	rubrerythrin [impo
698	60	5.8	3036	2	T18995	hypothetical prote	771	59.5	5.7	181	2	E97341	rubrerythrin [impo
699	60	5.8	98	2	F97245	probable HD superf	772	59.5	5.7	182	2	S19506	hypothetical prote
700	60	5.8	149	2	S47544	Bt11 protein - yea	773	59.5	5.7	202	2	T32159	hypothetical prote
701	60	5.8	180	2	T43451	hypothetical prote	774	59.5	5.7	204	2	T47457	hypothetical prote
702	60	5.8	217	2	S42772	ig kappa chain (m	775	59.5	5.7	239	2	B36036	cytochrome P450 2F
703	60	5.8	225	2	PC4203	ig kappa chain (m	776	59.5	5.7	260	1	R5T018	ribosomal protein
704	60	5.8	227	2	T04420	hypothetical prote	777	59.5	5.7	260	1	R5T018	ribosomal protein
705	60	5.8	238	2	T04420	ribonuclease (EC 3	778	59.5	5.7	260	2	T08016	probable expansin
706	60	5.8	238	2	I39731	hydrogenase chain	779	59.5	5.7	266	2	H83008	N-formylglutamate
707	60	5.8	238	2	AH1901	hydrogenase chain	780	59.5	5.7	266	2	H83008	secreted protein c
708	60	5.8	279	2	A27068	mannose 6-phospat	781	59.5	5.7	303	2	H97235	hypothetical prote
709	60	5.8	333	2	AF3528	flagellar m-ring p	782	59.5	5.7	309	2	AG1854	finger protein zfp
710	60	5.8	336	2	H81091	probable CDP-6-deo	783	59.5	5.7	315	2	S22316	acidic ribosomal p
711	60	5.8	338	2	A24567	isopenicillin N sy	784	59.5	5.7	321	1	R5UBP0	repetitive protein
712	60	5.8	338	2	S09312	isopenicillin N sy	785	59.5	5.7	333	1	R5UBP0	myristylated alani
713	60	5.8	348	2	A00638	dhhydroorotase (EC	786	59.5	5.7	335	2	H86158	hypothetical prote
714	60	5.8	350	2	B37316	connective tissue	787	59.5	5.7	337	2	T47079	folliculin - shree
715	60	5.8	356	2	B84183	serine proteinase	788	59.5	5.7	351	2	S45305	hypothetical prote
716	60	5.8	357	2	T01434	NADPH HC toxin red	789	59.5	5.7	351	2	S45305	CD44 antigen precu
717	60	5.8	392	2	A56229	lymphoid transcrip	790	59.5	5.7	353	2	I51572	maternal protein -
718	60	5.8	395	2	D70441	oxido/reductase ir	791	59.5	5.7	358	1	F64106	3-isopropylmalate
719	60	5.8	395	2	D64022	hypothetical prote	792	59.5	5.7	359	2	T18667	hypothetical prote
720	60	5.8	397	2	S09813	hypothetical prote	793	59.5	5.7	360	2	S60268	beta-mannosidase (
721	60	5.8	403	2	T09322	DNA polymerase pro	794	59.5	5.7	374	2	S40756	hypothetical prote
722	60	5.8	409	2	E69847	hypothetical prote	795	59.5	5.7	393	2	B86189	protein T25N20.9 [
723	60	5.8	427	2	B56229	lymphoid transcrip	796	59.5	5.7	397	2	A71114	probable ferredoxi
724	60	5.8	438	2	I38946	melanoma ubiquitou	797	59.5	5.7	412	2	S73631	UV protection prot
725	60	5.8	449	2	S41647	zinc finger 5 prot	798	59.5	5.7	422	2	AH1694	threonine dehydrat
726	60	5.8	452	2	C83998	acetyl-CoA carboxy	799	59.5	5.7	434	2	S73331	hypothetical prote
727	60	5.8	454	2	AF1217	Salmonella enteric	800	59.5	5.7	454	2	A70079	conserved hypoteth
728	60	5.8	454	2	T12539	hypothetical prote	801	59.5	5.7	465	2	A47023	S-layer protein -
729	60	5.8	483	2	T47422	cellulase-like pro	802	59.5	5.7	477	2	A47236	zinc-finger protei
730	60	5.8	497	2	JC5076	myc-associated zin	803	59.5	5.7	482	2	T29912	hypothetical prote
731	60	5.8	536	2	T01821	hypothetical prote	804	59.5	5.7	484	2	H96683	hypothetical prote
732	60	5.8	540	2	T14748	hypothetical prote	805	59.5	5.7	499	2	AD2262	amido-phosphoribosy
733	60	5.8	570	2	T00579	probable lacase [806	59.5	5.7	499	2	AC2068	cell death suppress
734	60	5.8	582	2	T12539	matrix metalloprot	807	59.5	5.7	535	2	JC5762	cytokine-inducibl
735	60	5.8	582	2	I38028	matrix metalloprot	808	59.5	5.7	544	2	S41093	triacylglycerol li
736	60	5.8	582	2	I38471	matrix metalloprot	809	59.5	5.7	563	2	A70038	L-lactate permease
737	60	5.8	643	2	T19199	hypothetical prote	810	59.5	5.7	564	2	T12489	hypothetical prote
738	60	5.8	707	2	S68858	finger protein - m	811	59.5	5.7	572	2	T16865	hypothetical prote
739	60	5.8	726	2	S22258	probable protein k	812	59.5	5.7	588	2	H95363	probable oxidoredu
740	60	5.8	749	2	T29859	mechanosensory pro	813	59.5	5.7	603	2	T08955	hypothetical prote
741	60	5.8	774	2	A39832	scabrous locus (sc	814	59.5	5.7	626	2	T49110	hypothetical prote
742	60	5.8	795	2	S33101	H4L protein - vari	815	59.5	5.7	658	2	D84969	probable receptor
743	60	5.8	795	2	T28525	hypothetical prote	816	59.5	5.7	686	2	T03123	DNA packaging prot
744	60	5.8	795	2	E72161	J4L protein - vari	817	59.5	5.7	693	2	H87125	hypothetical prote
745	60	5.8	815	2	T40524	hypothetical prote	818	59.5	5.7	750	2	AB0708	catalase (EC 1.11.
746	60	5.8	823	2	S14055	nucleoskeletal-lik	819	59.5	5.7	770	2	A54444	DNA-binding protei
747	60	5.8	940	2	B72120	valine-tRNA ligase	820	59.5	5.7	770	2	I49508	ISGF3 p91-related
748	60	5.8	940	2	F86502	alyl tRNA syntheta	821	59.5	5.7	783	2	B91124	probable isomerase
749	60	5.8	940	2	S73950	phosphotransferase	822	59.5	5.7	783	2	A85969	probable isomerase
750	60	5.8	953	2	B64083	hemoglobin-binding	823	59.5	5.7	783	2	B65096	hypothetical 88.3K
751	60	5.8	1016	2	H71460	probable outer mem	824	59.5	5.7	788	2	A37057	integrin beta-6 ch
752	60	5.8	1048	2	H87721	protein ZC123.2 [i	825	59.5	5.7	790	2	A35797	probable DNA-bindi
753	60	5.8	1051	2	A35761	cell surface glyco	826	59.5	5.7	801	2	H83737	glucosidase BH0704
754	60	5.8	1070	2	E71401	probable selenum-	827	59.5	5.7	827	1	XUECAG	glycerol-3-phospha
755	60	5.8	1106	2	S38783	integrin alpha cha	828	59.5	5.7	860	2	T22974	hypothetical prote
756	60	5.8	1174	2	T43051	protein kinase C (829	59.5	5.7	860	2	T22974	hypothetical prote
757	60	5.8	1190	2	F86677	pyruvate-flavodoxi	830	59.5	5.7	903	1	VGBEK1	glycoprotein B pre
758	60	5.8	1192	2	S69000	laminin gamma 2 ch	831	59.5	5.7	915	2	T21773	hypothetical prote
759	60	5.8	1208	2	C82779	hemolysin-type cal	832	59.5	5.7	919	2	E83212	probable sensor/re

833	59.5	5.7	927	2	T21772	hypothetical prote	906	59	5.7	499	2	I77466	potassium channel
834	59.5	5.7	939	2	H71532	valine-tRNA ligase	907	59	5.7	513	1	I58311	t-complex polysept
835	59.5	5.7	984	1	A34076	protein-tyrosine k	908	59	5.7	536	2	JC4521	hypothetical prote
836	59.5	5.7	1042	2	S41705	Evi1 protein - hum	909	59	5.7	541	2	T15259	involucrin - rat
837	59.5	5.7	1051	2	A31591	transcription regu	910	59	5.7	568	1	I61106	hypothetical prote
838	59.5	5.7	1051	2	A60191	oncogene Evi-1 - h	911	59	5.7	570	2	A97089	homeotic protein E
839	59.5	5.7	1101	2	G83637	hypothetical prote	912	59	5.7	584	2	B25682	adhesion of calyx
840	59.5	5.7	1173	2	T52575	gigantea protein f	913	59	5.7	594	2	T50764	adhesion of calyx
841	59.5	5.7	1182	2	T30189	myelin transcripti	914	59	5.7	594	2	T50765	two component sens
842	59.5	5.7	1221	2	A49457	fibulin-2 precurs	915	59	5.7	608	2	AD2590	hypothetical prote
843	59.5	5.7	1343	2	E90893	hypothetical prote	916	59	5.7	620	2	T16166	hypothetical prote
844	59.5	5.7	1343	2	D85724	hypothetical prote	917	59	5.7	630	2	JC5374	angiotensin-conver
845	59.5	5.7	1453	2	S41453	spike protein - ca	918	59	5.7	656	2	E97372	probable protein k
846	59.5	5.7	1513	2	A54895	mucin 2, intestina	919	59	5.7	657	2	T48228	endo-1,4-beta-xyla
847	59.5	5.7	1551	2	P66342	F9H16.4 protein -	920	59	5.7	661	1	S59633	lamin A - African
848	59.5	5.7	1629	2	T06461	DNA-binding protei	921	59	5.7	665	2	AE3348	exonuclease ABC c
849	59.5	5.7	1734	2	A54602	microtubule-associ	922	59	5.7	683	2	T37570	zinc finger protei
850	59.5	5.7	1876	2	T13801	phosphoinositide 3	923	59	5.7	716	1	VCFV2M	coat protein Vp1 -
851	59.5	5.7	1970	2	I38186	RNA polymerase II	924	59	5.7	723	2	A11290	beta-glucosidase
852	59.5	5.7	2364	2	A56577	microtubule-associ	925	59	5.7	724	2	T06668	brefeldin A-senait
853	59.5	5.7	2783	1	A14948	alpha-fetoprotein	926	59	5.7	825	1	EDBEXD	immediate-early pr
854	59.5	5.7	5825	2	T12117	polyprotein - fava	927	59	5.7	868	2	T22281	hypothetical prote
855	59.5	5.7	10223	2	T30225	polyketide synthas	928	59	5.7	884	2	G97273	protein F2K11.26 (
856	59	5.7	54	2	I39520	rubredoxin - Acine	929	59	5.7	1035	2	S59757	isoleucyl-tRNA syn
857	59	5.7	77	2	JC2431	cysteine-rich prot	930	59	5.7	1038	1	JC5757	DNA-directed DNA p
858	59	5.7	143	2	T04091	hypothetical prote	931	59	5.7	1121	2	T18222	HCRF2 protein - hu
859	59	5.7	171	2	A11280	hypothetical prote	932	59	5.7	1170	2	S52525	probable membrane
860	59	5.7	172	2	S06575	finger protein (cl	933	59	5.7	1186	2	G69708	chromosome segrega
861	59	5.7	185	2	S62699	photoassimilate-re	934	59	5.7	1257	2	T00486	serine/threonine-s
862	59	5.7	188	2	C97438	hypothetical prote	935	59	5.7	1323	2	PN0568	connectin 3B - chi
863	59	5.7	188	2	AP2656	conserved hypotet	936	59	5.7	1323	2	T30253	spalt protein - mo
864	59	5.7	216	2	T73913	polypeptide deform	937	59	5.7	1524	2	T30518	carbamoyl-phosphat
865	59	5.7	219	2	S52028	Ig kappa chain - m	938	59	5.7	1560	2	T00080	hypothetical prote
866	59	5.7	219	2	B84326	hypothetical prote	939	59	5.7	1608	2	A28182	hemolysin A - Serr
867	59	5.7	222	2	F86480	hypothetical prote	940	59	5.7	1905	2	T51553	Flexin - African c
868	59	5.7	265	2	S70247	hypothetical prote	941	59	5.7	2116	1	ZLVNSY	genome polyprotein
869	59	5.7	274	2	T16977	pectinesterase (EC	942	59	5.7	2485	1	H71621	serine/threonine-s
870	59	5.7	278	1	S25690	hupJ protein - Rho	943	59	5.7	3305	2	T18358	apolipoprotein prec
871	59	5.7	284	2	T52062	PRG-like protein	944	59	5.7	4544	1	S02332	alpha-2-macroglobu
872	59	5.7	304	2	T13127	protein gp41 - pha	945	59	5.7	5035	1	I46646	probable ferredoxi
873	59	5.7	304	2	C95372	probable integrase	946	59	5.7	108	2	C71114	probable ferredoxi
874	59	5.7	304	2	E95409	probable integrase	947	59	5.7	114	2	B49002	Ig kappa chain V r
875	59	5.7	305	1	BVCEA	UDP-3-O-[3-hydrox	948	58.5	5.6	135	2	B83461	hypothetical prote
876	59	5.7	305	2	AC0519	UDP-3-O-[3-hydrox	949	58.5	5.6	145	1	RMVTV	T-cell receptor be
877	59	5.7	305	2	D85492	UDP-3-O-[3-hydrox	950	58.5	5.6	154	2	S23044	T-cell receptor ga
878	59	5.7	314	2	F84886	probable C2H2-type	951	58.5	5.6	158	2	A40443	nerve growth facto
879	59	5.7	315	2	T16976	pectinesterase (EC	952	58.5	5.6	159	2	H86255	hypothetical prote
880	59	5.7	315	2	T16975	pectinesterase (EC	953	58.5	5.6	185	2	S54088	peptidylprolyl iso
881	59	5.7	315	2	C71344	probable apore coa	954	58.5	5.6	224	2	T05766	photosystem II oxy
882	59	5.7	316	2	AE3533	hypothetical prote	955	58.5	5.6	258	2	S22763	ribosomal protein
883	59	5.7	332	2	A38873	myristylated alani	956	58.5	5.6	260	2	S22641	hypothetical prote
884	59	5.7	334	2	T21033	hypothetical prote	957	58.5	5.6	265	2	F72618	hypothetical prote
885	59	5.7	347	2	D96590	translation initia	958	58.5	5.6	275	2	C70954	hydrogenase, chain
886	59	5.7	351	2	S71960	B-cell differentia	959	58.5	5.6	283	2	F69364	pyruvate formate-l
887	59	5.7	354	2	A32331	peptide chain rele	960	58.5	5.6	291	2	B82464	hypothetical prote
888	59	5.7	365	2	G85944	probable transcrip	961	58.5	5.6	304	2	C50453	hypothetical prote
889	59	5.7	373	2	T52182	probable isospart	962	58.5	5.6	315	2	A99192	nirv precursor (AF
890	59	5.7	390	2	AF1067	protein F12M16.13	963	58.5	5.6	315	2	A13094	nitrite reductase,
891	59	5.7	391	2	H96572	beta-ketoacyl-ACP	964	58.5	5.6	351	2	T25448	hypothetical prote
892	59	5.7	425	2	T44710	hypothetical prote	965	58.5	5.6	355	2	B26883	neural cell adhesi
893	59	5.7	433	2	T30239	En/Spm-like transp	966	58.5	5.6	356	2	T01435	NADPH HC toxin red
894	59	5.7	454	2	E84524	hypothetical prote	967	58.5	5.6	378	2	JH0134	creatinase (EC 3.5
895	59	5.7	455	2	S50391	hypothetical prote	968	58.5	5.6	384	2	A12962	cellulose synthesi
896	59	5.7	460	2	T33110	hypothetical prote	969	58.5	5.6	389	2	E98320	hypothetical prote
897	59	5.7	466	2	T01898	hypothetical prote	970	58.5	5.6	393	2	JN0533	finger protein pML
898	59	5.7	472	1	B53236	transcription fact	971	58.5	5.6	407	2	T66260	metalloproteinase
899	59	5.7	473	2	I49283	ADAM 4 protein pre	972	58.5	5.6	409	2	T19326	hypothetical prote
900	59	5.7	476	2	S21144	potassium channel	973	58.5	5.6	431	2	H81738	probable sodium-tr
901	59	5.7	477	2	S50738	QR11 protein - yea	974	58.5	5.6	442	1	V0FF2	vitellogenin II pr
902	59	5.7	480	2	H85112	hypothetical prote	975	58.5	5.6	448	2	S60961	hypothetical prote
903	59	5.7	486	2	T39456	zinc finger protei	976	58.5	5.6				
904	59	5.7	494	2	S74625	NADH-glutamate syn	977	58.5	5.6				
905	59	5.7					978	58.5	5.6				

979	58.5	5.6	451	2	D88395	protein F53A3.6 [i	1052	58	5.6	280	1	JQ1874	Bcl1 protein - toma
980	58.5	5.6	459	2	S76138	hypothetical prote	1053	58	5.6	283	2	T45871	hypothetical prote
981	58.5	5.6	487	2	S61993	probable membrane	1054	58	5.6	289	2	D96778	hypothetical prote
982	58.5	5.6	491	2	S95356	probable ABC trans	1055	58	5.6	293	2	D96560	hypothetical prote
983	58.5	5.6	492	2	S53111	emiatin synthetas	1056	58	5.6	297	2	A89451	protein T0469.4 [i
984	58.5	5.6	502	2	S56177	probable glutamate	1057	58	5.6	306	1	S39151	cyclin-suppressing
985	58.5	5.6	503	2	S56177	bone morphogenetic	1058	58	5.6	307	1	S53962	hypothetical prote
986	58.5	5.6	513	1	BMHU6	anthranilate synth	1059	58	5.6	323	2	C83282	hypothetical prote
987	58.5	5.6	520	2	AF0653	hypothetical prote	1060	58	5.6	328	2	S38138	transcription init
988	58.5	5.6	533	2	T13607	triacylglycerol li	1061	58	5.6	328	2	AF2469	F20D23.18 protein
989	58.5	5.6	544	2	S41091	triacylglycerol li	1062	58	5.6	331	2	B86307	finger protein (cl
990	58.5	5.6	544	2	S41092	triacylglycerol li	1063	58	5.6	336	2	S06578	finger protein ZNP
991	58.5	5.6	545	2	T36123	probable lysyl-trn	1064	58	5.6	337	2	S60520	conserved hypotet
992	58.5	5.6	549	2	S32987	hypothetical prote	1065	58	5.6	338	2	G69413	DNA-binding protei
993	58.5	5.6	559	2	B95120	site-specific reco	1066	58	5.6	353	2	T09887	transcription fact
994	58.5	5.6	559	2	F97989	site-specific reco	1067	58	5.6	358	1	A55973	Gfi-1-like protein
995	58.5	5.6	564	2	T40883	WD repeat protein	1068	58	5.6	366	2	JC7690	hypothetical prote
996	58.5	5.6	572	2	S72249	trithorax protein	1069	58	5.6	367	2	AF2494	dnaj protein limpo
997	58.5	5.6	609	2	A64432	modulation factor	1070	58	5.6	373	2	H97728	heat shock protein
998	58.5	5.6	623	2	B83399	quinoprotein alcoh	1071	58	5.6	389	2	A64402	E2 protein - human
999	58.5	5.6	689	2	B89898	hypothetical prote	1072	58	5.6	394	2	S36512	hypothetical prote
1000	58.5	5.6	690	2	S54775	cell size regulati	1073	58	5.6	394	2	C87498	hypothetical prote
1001	58.5	5.6	692	2	AC1234	DNA topoisomerase	1074	58	5.6	407	2	T20078	finger protein (cl
1002	58.5	5.6	692	2	A11596	DNA topoisomerase	1075	58	5.6	420	2	S06579	serine-tRNA ligase
1003	58.5	5.6	712	2	T33028	hypothetical prote	1076	58	5.6	427	2	F72026	seryl tRNA synthet
1004	58.5	5.6	728	2	A48830	probable transcrip	1077	58	5.6	427	2	D86599	acid phosphatase (
1005	58.5	5.6	736	2	A40096	platelet-endotheli	1078	58	5.6	436	2	T03866	morphogen Xhh prec
1006	58.5	5.6	756	2	C84682	hypothetical prote	1079	58	5.6	444	2	S56765	coproporphyrinogen
1007	58.5	5.6	764	2	T05768	subtilisin-like pr	1080	58	5.6	457	2	A64603	DNA-directed RNA p
1008	58.5	5.6	825	2	AC0039	glycerol-3-phospha	1081	58	5.6	478	2	S33886	AFS-binding factor
1009	58.5	5.6	827	2	H31256	glycerol-3-phospha	1082	58	5.6	482	2	S22654	metalloprotease </td
1010	58.5	5.6	827	2	D86097	glycerol-3-phospha	1083	58	5.6	484	2	JC8020	phosphoglycerate m
1011	58.5	5.6	853	1	IJBONC	neural cell adhesi	1084	58	5.6	508	2	G84339	hypothetical prote
1012	58.5	5.6	856	1	IJRTNC	neural cell adhesi	1085	58	5.6	510	2	T49308	finger protein (cl
1013	58.5	5.6	946	2	C96549	polymorphic oute	1086	58	5.6	536	2	S06548	probable aminopept
1014	58.5	5.6	946	2	D81594	polymorphic membra	1087	58	5.6	536	2	B83278	hypothetical prote
1015	58.5	5.6	946	2	C72075	polymorphic oute	1088	58	5.6	548	2	T27542	hypothetical prote
1016	58.5	5.6	976	2	T29583	hypothetical prote	1089	58	5.6	552	1	DEZFP	phosphoribosylamin
1017	58.5	5.6	1008	2	H85035	probable transposo	1090	58	5.6	555	1	SYQMA	malate synthase (E
1018	58.5	5.6	1093	2	I38533	AF17 protein - hum	1091	58	5.6	556	2	T46842	K+-transporting AT
1019	58.5	5.6	1099	2	T16822	hypothetical prote	1092	58	5.6	564	2	T15477	hypothetical prote
1020	58.5	5.6	1124	2	JX0293	zinc finger protei	1093	58	5.6	569	2	A43317	germ cell-less pro
1021	58.5	5.6	1170	1	TSRUP1	thrombospondin 1 p	1094	58	5.6	577	2	A60501	thrombospondulin pre
1022	58.5	5.6	1188	2	S50434	hypothetical prote	1095	58	5.6	583	2	T12576	probable phosphate
1023	58.5	5.6	1188	2	D86236	protein F14N23.5 [1096	58	5.6	593	2	JC7829	metal-responsive t
1024	58.5	5.6	1209	2	T52523	celE protein - Agr	1097	58	5.6	599	2	C86161	hypothetical prote
1025	58.5	5.6	1209	2	T52523	hypothetical prote	1098	58	5.6	600	2	S56744	mucin (clone pGM7-
1026	58.5	5.6	1210	2	A53183	epidermal growth f	1099	58	5.6	613	2	A39402	potassium channel
1027	58.5	5.6	1212	2	T44236	hypothetical prote	1100	58	5.6	616	2	B85508	hypothetical prote
1028	58.5	5.6	1231	2	C84716	hypothetical prote	1101	58	5.6	616	2	E90857	hypothetical prote
1029	58.5	5.6	1295	2	T24587	hypothetical prote	1102	58	5.6	624	2	S22703	voltage-gated pota
1030	58.5	5.6	1370	2	T19188	hypothetical prote	1103	58	5.6	627	2	T18772	hypothetical prote
1031	58.5	5.6	1373	2	J80095	gastric mucin MUC5	1104	58	5.6	631	2	S70908	transferrin-bindin
1032	58.5	5.6	1443	2	T31896	hypothetical prote	1105	58	5.6	639	2	S62567	hypothetical prote
1033	58.5	5.6	1484	2	T42632	breast cancer tumo	1106	58	5.6	644	2	D83971	stage V sporulatio
1034	58.5	5.6	1757	2	T05204	hypothetical prote	1107	58	5.6	654	1	E90055	fructose-bisphosph
1035	58.5	5.6	1920	2	T13893	gene hindsight pro	1108	58	5.6	654	2	T30136	hypothetical prote
1036	58.5	5.6	2210	1	RXPLC	genome polyprotein	1109	58	5.6	667	2	A48579	trophozoite surfac
1037	58.5	5.6	2342	2	T13412	hypothetical prote	1110	58	5.6	680	2	T29204	hypothetical prote
1038	58.5	5.6	2491	1	A28372	insulin-like growt	1111	58	5.6	728	2	S71467	diacylglycerol kin
1039	58.5	5.6	2570	2	T17451	finbriae-associate	1112	58	5.6	751	2	T48748	semaphorin E - mou
1040	58.5	5.6	2704	2	S09118	G surface protein	1113	58	5.6	823	2	T01362	probable myosin he
1041	58.5	5.6	2954	2	T14156	kinesin-related pr	1114	58	5.6	839	2	T45908	hypothetical prote
1042	58	5.6	119	2	A46356	tat protein - simi	1115	58	5.6	849	2	T46253	hypothetical prote
1043	58	5.6	128	2	A31799	hypothetical secre	1116	58	5.6	891	2	T19915	hypothetical prote
1044	58	5.6	140	2	S06574	finger protein (cl	1117	58	5.6	898	2	E96659	hypothetical prote
1045	58	5.6	164	2	A86802	prophage pi3 prote	1118	58	5.6	905	2	T38980	hypothetical prote
1046	58	5.6	169	2	S57138	hypothetical prote	1119	58	5.6	907	2	T27317	hypothetical prote
1047	58	5.6	215	2	S17987	adenylate kinase (1120	58	5.6	908	2	JN0819	transferrin-bindin
1048	58	5.6	259	1	ONGAOL	ovulation hormone	1121	58	5.6	937	2	S78561	cs3 pilin synthesi
1049	58	5.6	274	2	F70642	probable ribosomal	1122	58	5.6	1028	2	A56038	DNA-binding protei
1050	58	5.6	276	1	MPBOPL	myelin proteolipid	1123	58	5.6	1043	2	T13172	gag-like protein p
1051	58	5.6	278	2	T19813	hypothetical prote	1124	58	5.6	1069	2	T43280	nonsense-mediated

1125	58	5.6	1079	2	D71476	probable transcript	1198	57.5	5.6	466	2	A53764	beta2-chimerin, ce
1126	58	5.6	1094	2	C59434	KIAA1688 protein [1199	57.5	5.6	467	2	T40348	hypothetical prote
1127	58	5.6	1100	2	G84534	probable retroelem	1200	57.5	5.6	474	2	S16727	coenzyme F420 hydr
1128	58	5.6	1147	2	P86297	hypothetical prote	1201	57.5	5.6	478	1	KCRBS1	stromelysin 1 (EC
1129	58	5.6	1148	2	P86403	probable transposo	1202	57.5	5.6	479	2	T39634	conserved hypothet
1130	58	5.6	1171	2	T28701	probable polyketid	1203	57.5	5.6	480	1	A30055	trigramin precursor
1131	58	5.6	1212	2	JC2131	metabotropic glut	1204	57.5	5.6	494	2	A42170	zinc finger protei
1132	58	5.6	1213	2	S16356	ovo protein - frui	1205	57.5	5.6	495	2	C95144	glucose-6-phosphat
1133	58	5.6	1214	2	JC7259	Smad interacting p	1206	57.5	5.6	495	2	A98012	glucose-6-phosphat
1134	58	5.6	1216	2	S46177	probable Ca2+-tran	1207	57.5	5.6	496	2	T08674	probable finger pr
1135	58	5.6	1236	2	B36329	hypothetical prote	1208	57.5	5.6	511	2	T17298	hypothetical prote
1136	58	5.6	1296	2	T16859	hypothetical prote	1209	57.5	5.6	535	2	S58224	oestrogen receptor
1137	58	5.6	1394	2	A35626	transforming growt	1210	57.5	5.6	544	2	A69503	conserved hypothet
1138	58	5.6	1462	1	A59809	probable multifunc	1211	57.5	5.6	546	2	T46718	probable farnesyl
1139	58	5.6	1475	2	S42718	nuclear pore compl	1212	57.5	5.6	575	1	THHUB	thrombomodulin pre
1140	58	5.6	1613	2	G64488	reverse gyrase (in	1213	57.5	5.6	595	2	C88482	protein COSD11.7 [
1141	58	5.6	1737	2	T00209	MEGF8 protein - hu	1214	57.5	5.6	607	2	A43776	debrin E2 - chick
1142	58	5.6	1801	1	MMRTS	laminin beta-2 cha	1215	57.5	5.6	616	2	T46292	hypothetical prote
1143	58	5.6	1942	2	B71426	hypothetical prote	1216	57.5	5.6	618	2	F84855	hypothetical prote
1144	58	5.6	1952	2	T48814	hypothetical prote	1217	57.5	5.6	624	2	S41688	DNA-binding protei
1145	58	5.6	2077	2	T43991	large tegument pro	1218	57.5	5.6	628	2	G82902	hypothetical prote
1146	58	5.6	2111	2	T15390	hypothetical prote	1219	57.5	5.6	639	2	JC1391	dnak-type molecula
1147	58	5.6	2531	2	S18188	notch protein homo	1220	57.5	5.6	654	2	T10772	calpastatin - rat
1148	58	5.6	2531	2	A46019	notch-1 protein -	1221	57.5	5.6	655	2	A59430	hypothetical prote
1149	58	5.6	2533	2	T28675	alpha-51D immobili	1222	57.5	5.6	661	1	OMRTA1	acyl-CoA oxidase (
1150	58	5.6	2533	2	T28674	alpha-51D immobili	1223	57.5	5.6	686	2	S28042	hemin receptor pre
1151	58	5.6	3507	2	T34513	hypothetical prote	1224	57.5	5.6	693	2	A12584	hypothetical prote
1152	57.5	5.6	110	2	B70601	hypothetical prote	1225	57.5	5.6	697	2	T26707	hypothetical prote
1153	57.5	5.6	120	2	S42268	ig kappa chain V r	1226	57.5	5.6	703	2	H87360	hypothetical prote
1154	57.5	5.6	123	1	C44212	structural protein	1227	57.5	5.6	713	2	A35502	major surface-labe
1155	57.5	5.6	133	2	S23230	ig kappa chain pre	1228	57.5	5.6	725	2	S60712	band-6-protein - h
1156	57.5	5.6	133	2	S40324	ig kappa chain V r	1229	57.5	5.6	728	2	H97366	ribonucleotide red
1157	57.5	5.6	139	2	H75177	hydrogenase expres	1230	57.5	5.6	741	2	S43768	transcription acti
1158	57.5	5.6	163	1	RHSC1	ribosomal protein	1231	57.5	5.6	742	2	T46488	hypothetical prote
1159	57.5	5.6	163	2	A84267	50S ribosomal prot	1232	57.5	5.6	767	1	S75875	ribonucleoside-dip
1160	57.5	5.6	170	2	C86652	hypothetical prote	1233	57.5	5.6	776	2	B41704	genome polypotein
1161	57.5	5.6	171	2	A86800	prophage pi3 prote	1234	57.5	5.6	776	2	A41704	conserved hypothet
1162	57.5	5.6	173	2	T51098	hypothetical prote	1235	57.5	5.6	782	2	AF0179	hypothetical prote
1163	57.5	5.6	213	2	T36929	ZNF80 homolog - gr	1236	57.5	5.6	794	2	S58376	hypothetical prote
1164	57.5	5.6	222	2	C84391	hypothetical prote	1237	57.5	5.6	847	1	IJHUBD	desmocollin 3b pre
1165	57.5	5.6	235	2	S20000	ig light chain pre	1238	57.5	5.6	876	2	PC2219	polypeptide - hepa
1166	57.5	5.6	235	2	S55883	CCHH finger protei	1239	57.5	5.6	887	2	C86433	CDS protein F9L11.
1167	57.5	5.6	253	2	S28943	cuticle protein, p	1240	57.5	5.6	894	2	T01385	probable phosphop
1168	57.5	5.6	277	2	I83570	hemk protein (EC 1	1241	57.5	5.6	901	1	IJHUDA	desmocollin 3a pre
1169	57.5	5.6	284	2	T41285	hypothetical prote	1242	57.5	5.6	902	2	A49227	sialidase - Actino
1170	57.5	5.6	289	2	C87019	hypothetical prote	1243	57.5	5.6	922	2	T23573	hypothetical prote
1171	57.5	5.6	296	2	A45447	zinc finger (alter	1244	57.5	5.6	982	1	GNLJH2	pol polypotein -
1172	57.5	5.6	312	2	T46255	hypothetical prote	1245	57.5	5.6	1029	2	T02576	hypothetical prote
1173	57.5	5.6	316	2	A05043	finger protein xfp	1246	57.5	5.6	1043	2	A56037	DNA-binding protei
1174	57.5	5.6	320	2	E98176	hypothetical prote	1247	57.5	5.6	1067	2	AB0260	probable phage hos
1175	57.5	5.6	320	2	AG3110	dehydrogenase Atu4	1248	57.5	5.6	1088	2	B34106	protein kinase (EC
1176	57.5	5.6	328	2	G90159	conserved hypothet	1249	57.5	5.6	1102	2	S65235	probable membrane
1177	57.5	5.6	338	2	AF2339	hypothetical prote	1250	57.5	5.6	1114	2	S50222	deltasg1 - chicken
1178	57.5	5.6	339	2	T00632	hypothetical prote	1251	57.5	5.6	1117	2	JC4934	deltacrystatin/E
1179	57.5	5.6	351	2	I68620	rod outer segment	1252	57.5	5.6	1126	2	A96032	probable two-compo
1180	57.5	5.6	366	2	T44174	DNA polymerase pro	1253	57.5	5.6	1157	2	F97255	fusion of alpha-g1
1181	57.5	5.6	371	2	C84254	hypothetical prote	1254	57.5	5.6	1177	2	T16594	hypothetical prote
1182	57.5	5.6	376	2	T48245	hypothetical prote	1255	57.5	5.6	1191	2	S35305	zinc finger protei
1183	57.5	5.6	384	2	AC1048	hypothetical prote	1256	57.5	5.6	1195	1	C54440	DNA repair protei
1184	57.5	5.6	391	2	A49645	probable 4fe-48 bi	1257	57.5	5.6	1437	2	S07430	M polypotein prec
1185	57.5	5.6	392	2	A49645	transcription fact	1258	57.5	5.6	1445	2	T14913	CA78 protein - yea
1186	57.5	5.6	394	2	T43987	pp41, pol processi	1259	57.5	5.6	1627	2	S65464	pregnancy-associat
1187	57.5	5.6	399	2	T20419	hypothetical prote	1260	57.5	5.6	1678	2	T35547	hypothetical prote
1188	57.5	5.6	399	2	T20455	hypothetical prote	1261	57.5	5.6	1970	1	S21054	DNA-directed RNA p
1189	57.5	5.6	412	2	T23385	hypothetical prote	1262	57.5	5.6	2132	1	A55182	aggreacan precursor
1190	57.5	5.6	412	2	D69525	arylsulfatase regu	1263	57.5	5.6	2481	2	A43908	fibronectin - Afri
1191	57.5	5.6	414	1	HYRSAC	atrolysin C (EC 3	1264	57.5	5.6	2531	2	T31070	notch homolog - se
1192	57.5	5.6	414	2	S41608	atrolysin B (EC 3	1265	57.5	5.6	3005	2	T08841	polypotein - dour
1193	57.5	5.6	428	2	S58735	homocitrate syntha	1266	57.5	5.6	3341	1	A42996	genome polypotein
1194	57.5	5.6	430	2	H69364	aspartyl-tRNA synt	1267	57	5.5	74	2	A44366	zinc finger protei
1195	57.5	5.6	440	1	S67674	homocitrate syntha	1268	57	5.5	77	1	GRTT1	cysteine-rich inte
1196	57.5	5.6	453	2	G69494	DNA helicase homol	1269	57	5.5	98	2	B90828	hypothetical prote
1197	57.5	5.6	454	2	T02680	hypothetical prote	1270	57	5.5	98	2	H85685	unknown protein en

1271	57	5.5	106	1	TNLJS2	trans-activating t	1344	57	5.5	499	2	A33814	potassium channel
1272	57	5.5	107	2	S24290	Ig kappa chain V r	1345	57	5.5	499	2	D75416	prolyl-L-lysine synthase
1273	57	5.5	133	1	A69053	conserved hypothet	1346	57	5.5	500	1	EPFF	zip protein precursor
1274	57	5.5	135	1	RWHUV	T-cell receptor be	1347	57	5.5	502	2	AD3563	erythritol-4-phosph
1275	57	5.5	149	2	D69401	hypothetical protei	1348	57	5.5	503	2	T51711	probable isochoris
1276	57	5.5	154	2	JC4588	RNA-binding protei	1349	57	5.5	503	2	D96776	hypothetical prote
1277	57	5.5	159	2	S34134	ribosomal protein	1350	57	5.5	515	2	D90108	chaperonin-contain
1278	57	5.5	166	2	D83230	hypothetical prote	1351	57	5.5	526	2	T13687	hypothetical prote
1279	57	5.5	171	2	AG2730	hypothetical prote	1352	57	5.5	529	2	S12787	potassium channel
1280	57	5.5	171	2	G97511	hypothetical prote	1353	57	5.5	529	2	A71899	hypothetical prote
1281	57	5.5	174	2	A35383	superoxide dismuta	1354	57	5.5	545	2	AC1914	hypothetical prote
1282	57	5.5	180	2	T41300	protein involved i	1355	57	5.5	561	2	T27318	protein-tyrosine-p
1283	57	5.5	193	1	UN0728	hypothetical prote	1356	57	5.5	566	1	B41648	hypothetical prote
1284	57	5.5	197	2	C82601	hypothetical prote	1357	57	5.5	571	2	E96550	hypothetical prote
1285	57	5.5	198	2	T25436	hypothetical prote	1358	57	5.5	572	2	AC0506	probable sulfatase
1286	57	5.5	205	2	S68435	aralkylamine N-ace	1359	57	5.5	583	2	C72544	probable glycyl-tr
1287	57	5.5	209	2	S51480	drought-induced pr	1360	57	5.5	583	2	T17326	hypothetical prote
1288	57	5.5	213	2	G69850	hypothetical prote	1361	57	5.5	589	2	I38598	zinc finger protei
1289	57	5.5	216	2	A82635	bacteriophage repr	1362	57	5.5	610	2	A35046	E-selectin precurs
1290	57	5.5	216	2	G97417	hypothetical prote	1363	57	5.5	611	2	S56278	DNA-directed DNA p
1291	57	5.5	222	2	A49995	salt-mediated kill	1364	57	5.5	625	2	T37604	phosphotransferase
1292	57	5.5	227	2	H90527	glucose inhibited	1365	57	5.5	625	2	T37604	probable transcrip
1293	57	5.5	238	1	JX0127	ribonuclease M (EC	1366	57	5.5	626	2	JQ2322	starch synthase (E
1294	57	5.5	238	1	H64707	conserved hypothet	1367	57	5.5	632	2	H70339	NADH2 dehydrogenas
1295	57	5.5	241	2	A42299	hypothetical prote	1368	57	5.5	647	2	S36517	E1 protein - human
1296	57	5.5	243	2	B33329	cysteine-rich secr	1369	57	5.5	650	2	H81708	hypothetical prote
1297	57	5.5	244	2	JC80139	CB58 protein - pig	1370	57	5.5	655	2	S51884	probable protein k
1298	57	5.5	252	2	T10697	immature seed prot	1371	57	5.5	664	2	S02116	RNA helicase MSB1
1299	57	5.5	255	1	SNRUC8	proteasome endopep	1372	57	5.5	670	2	A25001	catalase (EC 1.11.
1300	57	5.5	255	1	SNRUC8	proteasome endopep	1373	57	5.5	711	2	S70660	transferrin-bindin
1301	57	5.5	263	2	E64860	hypothetical prote	1374	57	5.5	723	2	H85092	hypothetical prote
1302	57	5.5	286	2	F96720	unknown protein, 5	1375	57	5.5	734	2	T02820	probable membrane
1303	57	5.5	310	2	T20535	hypothetical prote	1376	57	5.5	750	2	T19080	hypothetical prote
1304	57	5.5	314	2	H71802	probable outer mem	1377	57	5.5	766	2	S69657	hypothetical prote
1305	57	5.5	317	1	RSMS10	acidic ribosomal p	1378	57	5.5	777	2	C41830	DNA primase - phag
1306	57	5.5	322	2	T14625	hypothetical prote	1379	57	5.5	788	1	S15239	anthranilate synth
1307	57	5.5	323	2	D90413	thioredoxin reduct	1380	57	5.5	810	2	A44054	orf1 protein - Jun
1308	57	5.5	323	2	T02617	hypothetical prote	1381	57	5.5	830	1	B48723	replication licens
1309	57	5.5	327	2	F71800	ABC transporter, A	1382	57	5.5	830	1	B48723	hypothetical prote
1310	57	5.5	330	2	D84914	hypothetical prote	1383	57	5.5	885	1	WMBX3L	ribonucleoside-dip
1311	57	5.5	338	2	C64099	fructose-6-phosph	1384	57	5.5	896	2	I45858	desmocolin - bovi
1312	57	5.5	343	2	H83817	transcription repr	1385	57	5.5	898	2	T26577	hypothetical prote
1313	57	5.5	344	2	A90040	hypothetical prote	1386	57	5.5	973	2	B89009	protein T27C4.4 [i
1314	57	5.5	355	2	A00921	UDP-N-acetylglucos	1387	57	5.5	1003	1	PVYZAM	spheroidin precurs
1315	57	5.5	360	2	S48365	hypothetical prote	1388	57	5.5	1020	2	S05944	neuronal cell surf
1316	57	5.5	364	1	ADCHB	fructose-bisphosph	1389	57	5.5	1021	2	A57112	contactin precursor
1317	57	5.5	365	1	FCBCE2	translation releas	1390	57	5.5	1045	2	A29840	serine proteinase
1318	57	5.5	365	2	C91099	peptide chain rele	1391	57	5.5	1078	2	A56715	calcium receptor (
1319	57	5.5	368	2	T15492	hypothetical prote	1392	57	5.5	1106	2	T29496	hypothetical prote
1320	57	5.5	379	2	A42964	guanine nucleotide	1393	57	5.5	1129	2	T19779	pyruvate carboxyla
1321	57	5.5	381	1	SUBS1	subtilisin (EC 3.4	1394	57	5.5	1195	2	T43735	probable RNA-direc
1322	57	5.5	381	1	SUBS1	subtilisin (EC 3.4	1395	57	5.5	1215	2	T11660	protein F52G2.2 [i
1323	57	5.5	381	2	JH0778	subtilisin (EC 3.4	1396	57	5.5	1265	2	F88886	probable SNF2 subf
1324	57	5.5	381	2	I51174	Ig heavy chain - R	1397	57	5.5	1339	2	A84683	hypothetical prote
1325	57	5.5	392	2	H84679	hypothetical prote	1398	57	5.5	1398	2	T13741	hypothetical prote
1326	57	5.5	395	2	T47122	cell division prot	1399	57	5.5	1410	2	T47137	bacillopeptidase F
1327	57	5.5	400	1	NOHSM	phosphopyruvate hy	1400	57	5.5	1433	1	A36734	protein-tyrosine-p
1328	57	5.5	400	2	S74909	transposase slr206	1401	57	5.5	1442	2	S72441	patched protein -
1329	57	5.5	442	2	D87594	genetic exchange p	1402	57	5.5	1442	2	T18538	probable retroelem
1330	57	5.5	445	2	AF3394	proline-lysine ligas	1403	57	5.5	1461	2	E84589	protein T22F7.3 [i
1331	57	5.5	447	1	WNADMA	early E1B 50K prot	1404	57	5.5	1522	2	H88380	hypothetical prote
1332	57	5.5	449	1	NBESSA	glucose-6-phosphat	1405	57	5.5	1557	2	T28811	hypothetical prote
1333	57	5.5	458	2	S71523	polygalacturonase	1406	57	5.5	1589	2	T42233	submaxillary mucin
1334	57	5.5	461	2	H83882	hypothetical prote	1407	57	5.5	1717	1	A45558	epidermal growth f
1335	57	5.5	462	1	H64614	conserved hypothet	1408	57	5.5	2064	2	G82562	bacteriocin XF2407
1336	57	5.5	464	2	I60194	calcitonin-like re	1409	57	5.5	2136	2	A05037	hypothetical prote
1337	57	5.5	469	2	A03387	serine-tRNA ligase	1410	57	5.5	2139	2	A35672	crumbs protein - f
1338	57	5.5	472	2	E98020	hypothetical prote	1411	57	5.5	2248	2	A35938	profilaggrin - hum
1339	57	5.5	490	2	G71563	hypothetical prote	1412	57	5.5	2517	2	S58380	probable RNA-direc
1340	57	5.5	492	2	T07492	H+-transporting tw	1413	57	5.5	2761	2	T21064	hypothetical prote
1341	57	5.5	498	1	PWRZB	H+-transporting tw	1414	57	5.5	2907	2	A57278	fibrillin-2 precur
1342	57	5.5	499	2	A48672	delayed rectifier	1415	57	5.5	3071	2	T50345	vacuolar protein 8
1343	57	5.5	499	2	I84204	potassium channel	1416	56.5	5.5	91	2	H42075	finger protein (cl

1417 56.5 110 2 S19454 probable membrane
1418 56.5 120 2 S42267 Ig kappa chain V r
1419 56.5 133 2 T40279 hypothetical HIT-f
1420 56.5 140 2 S26384 hypothetical prote
1421 56.5 142 2 S22902 Ig kappa chain V r
1422 56.5 149 2 A29942 developmental cont
1423 56.5 157 2 E83629 hypothetical prote
1424 56.5 162 2 E87094 probable phosphope
1425 56.5 163 2 A23265 hypothetical prote
1426 56.5 164 2 T14187 hypothetical prote
1427 56.5 180 2 AG0796 NADH2 dehydrogenas
1428 56.5 180 2 F85868 NADH dehydrogenase
1429 56.5 180 2 G64999 NADH dehydrogenase
1430 56.5 181 2 E91024 NADH dehydrogenase
1431 56.5 181 2 S65230 hypothetical prote
1432 56.5 207 2 I38602 zinc finger protei
1433 56.5 214 2 S1405 synaptobrevin SBC2
1434 56.5 222 2 F90518 conserved hypothet
1435 56.5 224 2 B17883 hypothetical prote
1436 56.5 241 2 E81264 probable transcrip
1437 56.5 241 2 B86105 probable transcrip
1438 56.5 246 2 T19850 hypothetical prote
1439 56.5 253 2 S77778 probable NH(3)-dep
1440 56.5 254 2 T02078 photosystem II oxy
1441 56.5 259 2 E84886 probable beta-expa
1442 56.5 261 2 T11253 cytochrome-c oxida
1443 56.5 262 2 S62756 succinate dehydrog
1444 56.5 262 2 T14610 hypothetical prote
1445 56.5 277 2 S14431 knob-associated hi
1446 56.5 278 2 T44412 ABC transporter (A
1447 56.5 290 2 C97198 methyl-accepting c
1448 56.5 294 2 S76540 hypothetical prote
1449 56.5 295 1 S29399 homeotic protein m
1450 56.5 296 2 C87505 histone deacetylase
1451 56.5 299 2 T46690 CD80 precursor - r
1452 56.5 299 2 S56749 functional adhesio
1453 56.5 307 1 S18523 fructokinase (EC 2
1454 56.5 308 2 T29756 hypothetical prote
1455 56.5 322 2 A70661 hypothetical prote
1456 56.5 331 2 A69794 hypothetical prote
1457 56.5 339 2 AG2041 queuine tRNA-ribos
1458 56.5 348 2 H81186 probable alcohol d
1459 56.5 352 2 T04270 hypothetical prote
1460 56.5 352 2 T47820 hypothetical prote
1461 56.5 352 2 F69220 sensory transducti
1462 56.5 367 2 S05582 finger protein (cl
1463 56.5 370 2 S49008 fork head protein
1464 56.5 374 2 S41758 heat shock protein
1465 56.5 374 2 C97058 molecular chaperon
1466 56.5 376 1 RGRY43 cell division cont
1467 56.5 383 2 G71442 hypothetical prote
1468 56.5 389 2 A28672 rhizopuspepsin (EC
1469 56.5 399 2 F83633 hypothetical prote
1470 56.5 400 2 AE2889 acriflavin resistat
1471 56.5 403 2 H87569 hypothetical prote
1472 56.5 410 2 B97665 membrane fusion pr
1473 56.5 420 2 F89945 histidyl-tRNA synt
1474 56.5 420 2 F96018 probable adenylate
1475 56.5 425 2 H84348 hypothetical prote
1476 56.5 426 2 H84846 probable polygalac
1477 56.5 443 2 B53764 beta2-chimerin, ce
1478 56.5 450 2 D18916 hypothetical prote
1479 56.5 450 2 T10926 probable serine pr
1480 56.5 453 2 S38986 hydroxymethylgluta
1481 56.5 453 2 A43765 stsl+ protein - fi
1482 56.5 461 2 D96757 hypothetical prote
1483 56.5 464 2 D71219 probable L-asparta
1484 56.5 467 2 A43357 pancreatic lipase-
1485 56.5 473 2 A54494 knob-associated hi
1486 56.5 476 1 KCRTS2 stromelysin 2 (EC
1487 56.5 480 2 G75313 molybdate metaboli
1488 56.5 495 2 A85491 meso-diaminopimela
1489 56.5 498 1 PWSPB H+-transporting tw

1490 56.5 516 2 S42093 cellulose 1,4-beta
1491 56.5 518 2 T13652 hypothetical prote
1492 56.5 521 2 T08064 alanine transamina
1493 56.5 534 2 T39903 serine-rich protei
1494 56.5 546 2 G72210 hypothetical prote
1495 56.5 546 2 JC4798 seizure-related me
1496 56.5 550 2 T37579 Digeorge syndrome
1497 56.5 552 2 F82813 inner membrane pro
1498 56.5 554 2 T33294 proline-tRNA ligas
1499 56.5 569 2 G81400 phosphomannomutase
1500 56.5 587 2 T41173

ALIGNMENTS

RESULT 1

AF0711 conserved hypothetical protein STY1824 [imported] - Salmonella enterica subsp. enterica
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AF0711
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AF0711
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-147 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD02063.1; PID:gl65029900; GSPDB:GN00176
C:Genetics:
A:Gene: STY1824
C:Superfamily: hypothetical protein YCL033c

Query Match 41.4%; Score 428.5; DB 2; Length 147;
Best Local Similarity 51.0%; Pred. No. 6.9e-32;
Matches 73; Conservative 30; Mismatches 37; Indels 3; Gaps 1;

QY 38 KKNCKVWFSPQ---QELRRKRLTFLQYVHTQKGTSAFEGYTHHKDPGKYKCVGCTPLF 94

Db 5 KVRCEQMANQPSASELKKLSEMQFYVTDRTGTPPTGRLLNKRDGVYHCLVCDTPLF 64

QY 95 KSETKFDGSGSWPFDHVINSEAITFTDPSYGMHVRVETSCQCAHLGHIHFDGPRPTG 154

Db 65 HSHTKYDSGCGWPSFYQVSEAIRYIDDFSHGQVRVIRCGNCDAHLGHVFPDGPQPTG 124

QY 155 KRYCINSALSFTPADSSGTAEG 177

Db 125 ERYCVNSASLAFSDKXGDLKLG 147

RESULT 2

H96576 hypothetical protein P22G10.17 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: H96576

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Frazer, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

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A:Accession: H96576
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-202 <STO>
A:Cross-references: UNIPROT:Q9C8M2; GB:AE005173; NID:g10645339; PIDN:AAG21459.1; GSPDB:G
C:Genetics:
A:Gene: P22G10.17
A:Map position: 1

Query Match      40.8%; Score 423; DB 2; Length 202;
Best Local Similarity 48.6%; Pred. No. 3.1e-31;
Matches 84; Conservative 25; Mismatches 52; Indels 12; Gaps 2;

Qy  5  RTLPRLSLCLSLCLCLAAALGSAQSGCRD-----KKCKVVFSSQQLRKLTLPLOY 59
Db  35  RSLSKPRNLSLV-----YSGSSSSSPKPDNVQAEKNEFASLSENEWKRLTPEQY 87

Qy  60  HVTQKGTSAFEGEYTHHKDPGYKVCVCGTLPFKSETKFDGSGWPSFHDVINSIAIT 119
Db  88  YITQKGTERTAFTEYWNKTPGVYNCVCCDTPLFDSSTKFDSTGTFPSYYQPIGNVKT 147

Qy  120  FTDDFSYGMHRVETSCQCGAHLGHIFDDGPRPTGKRYCINSAAALSFTPADSS 172
Db  148  KDLSLIIPMPQEVVCAVCAHGHVFDGPRPTGKRYCLNSAALKLNALEKT 200

RESULT 3
A69195
transcription regulator - Methanobacterium thermoautotrophicum (strain Delta H)
C:Species: Methanobacterium thermoautotrophicum
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: A69195
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Qi, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwan, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funcu
A:Reference number: A69000; MUID:98037514; PMID:9371463
A:Accession: A69195
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-151 <MTH>
A:Cross-references: UNIPROT:O26807; GB:AE000850; GB:AE000666; NID:g2621794; PIDN:AAB8521
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH711
C:Superfamily: hypothetical protein YCL033c

Query Match      39.3%; Score 407; DB 2; Length 151;
Best Local Similarity 55.3%; Pred. No. 6.5e-30;
Matches 73; Conservative 18; Mismatches 41; Indels 0; Gaps 0;

Qy  42  KVFSSQQLRKLTLPLOYHVTQKGTSAFEGEYTHHKDPGYKVCVCGTLPFKSETKFD 101
Db  20  RIELSDDEWREILOPEARVARKAGTEPPFTGKYHLDHDDGYRICICGDTLFDSETKFD 79

Qy  102  SSGSWPSFHDVINSIAITFTDDFSYGMHRVETSCQCAHGHIFDDGPRPTGKRYCINS 161
Db  80  SGTGWPSFYDVVSEHNKLRDRSLGMVRCVLCARCDALHGHVFDGPRPTGKRYCINS 139

Qy  162  AALSFTPADSSG 173
Db  140  AALKFIPRDQIG 151

RESULT 4
A83293
conserved hypothetical protein PA2827 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: A83293
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
```

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.: Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: A83293
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-132 <STO>
A:Cross-references: UNIPROT:Q9I016; GB:AE004709; GB:AE004091; NID:g9948904; PIDN:AAG0621
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA2827
C:Superfamily: hypothetical protein YCL033c

Query Match      39.2%; Score 406; DB 2; Length 132;
Best Local Similarity 57.9%; Pred. No. 7e-30;
Matches 70; Conservative 17; Mismatches 34; Indels 0; Gaps 0;

Qy  51  RKRLTLPLOYHVTQKGTSAFEGEYTHHKDPGYKVCVCGTLPFKSETKFDGSGWPSFH 110
Db  12  REELTEQFHCRLGTERAFSGEYHATKTPGTYHCTCCGTALFDSDAKYDSSGWSYF 71

Qy  111  DVINSEAITFTDDFSYGMHRVETSCQCAHGHIFDDGPRPTGKRYCINSAAALSFTPAD 170
Db  72  QPVDAEAVRELDLDFSHGMHRIEVRGCRDAHLGHVFPDGPRTGLRYCINSASLKYPRE 131

Qy  171  S 171
Db  132  S 132

RESULT 5
B64938
hypothetical protein b1778 - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: B64938
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: B64938
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-137 <BLAT>
A:Cross-references: UNIPROT:P39903; GB:AE000272; GB:U00096; NID:gl788067; PIDN:AAC74848.1
A:Experimental source: strain K-12, substrain MG1655
C:Superfamily: hypothetical protein YCL033c

Query Match      39.1%; Score 405; DB 1; Length 137;
Best Local Similarity 50.0%; Pred. No. 9e-30;
Matches 66; Conservative 27; Mismatches 39; Indels 0; Gaps 0;

Qy  46  SQBELRKLTLPLOYHVTQKGTSAFEGEYTHHKDPGYKVCVCGTLPFKSETKFDGSG 105
Db  6  SARELKKNLSEMPYVTQNHGTEPPFTGRLLNKRGDGVHCLICDAPLFHSQTKYDSGCG 65

Qy  106  WPSFHDVINSIAITFTDDFSYGMHRVETSCQCAHGHIFDDGPRPTGKRYCINSAAALS 165
Db  66  WPSFPVPVSESIYIKDLSHGMRQIRGCNCDAHLGHVFPDGPQPTGTRYCVNSASLR 125

Qy  166  FTPADSSGTAEG 177
Db  126  FTDGNGERING 137

RESULT 6
G90939
hypothetical protein ECs2487 [imported] - Escherichia coli (strain O157:H7, substrain R1
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: G90939
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GenCore version 5.1.6
 OM protein - protein search, using sw model
 Run on: September 3, 2005, 02:22:32 ; Search time 165 Seconds
 (without alignments)
 450.048 Million cell updates/sec

Title: US-10-245-013-48
 Perfect score: 1036
 Sequence: 1 MSPRTLPRPLSLCLSLC.....GTABGGGVASPAQADKAEL 192
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 Total number of hits satisfying chosen parameters: 2105692
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%

Database :
 Listing first 1500 summaries
 1: Geneseq16Dec04:*
 2: Geneseq1990s:*
 3: Geneseq2000s:*
 4: Geneseq2001s:*
 5: Geneseq2002s:*
 6: Geneseq2003as:*
 7: Geneseq2003bs:*
 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AM39736	standard; protein; 192 AA.				
DE	Human polypeptide SEQ ID NO 2881.					
PN	WO200153312-A1.					
PD	26-JUL-2001.					
PA	(HYSE-) HYSEQ INC.					
Query Match	100.0%;	Score 1036;	DB 4;	Length 192;		
Best Local Similarity	100.0%;	Pred. No. 7.7e-99;				
RESULT 2						
ID	ABG34053	standard; protein; 192 AA.				
DE	Human Pro peptide #24.					
PN	WO200224888-A2.					
PD	28-MAR-2002.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1036;	DB 5;	Length 192;		
Best Local Similarity	100.0%;	Pred. No. 7.7e-99;				
RESULT 3						
ID	ADA01316	standard; protein; 192 AA.				
DE	Human PRO polypeptide #24.					
PN	US2003068779-A1.					
PD	10-APR-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1036;	DB 6;	Length 192;		
Best Local Similarity	100.0%;	Pred. No. 7.7e-99;				
RESULT 4						
ID	ADA343745	standard; protein; 192 AA.				
DE	Human secreted/transmembrane polypeptide PRO4487.					
PN	US2003064474-A1.					
PD	03-APR-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1036;	DB 6;	Length 192;		
Best Local Similarity	100.0%;	Pred. No. 7.7e-99;				
RESULT 5						
ID	ADA43513	standard; protein; 192 AA.				
DE	Human secreted/transmembrane polypeptide PRO4487.					
PN	US2003073196-A1.					
PD	17-APR-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1036;	DB 6;	Length 192;		
Best Local Similarity	100.0%;	Pred. No. 7.7e-99;				
RESULT 6						
ID	ADA01188	standard; protein; 192 AA.				

DE Human PRO polypeptide #24.
 PN US2003068782-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1036; DB 6; Length 192;
 Best Local Similarity 100.0%; Pred. No. 7.7e-99;
 RESULT 7
 ID ADA01072 standard; protein; 192 AA.
 DE Human secreted/transmembrane polypeptide PRO4487.
 PN US2003068780-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1036; DB 7; Length 192;
 Best Local Similarity 100.0%; Pred. No. 7.7e-99;
 RESULT 8
 ID ADA43629 standard; protein; 192 AA.
 DE Human secreted/transmembrane polypeptide PRO4487.
 PN US2003073190-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1036; DB 7; Length 192;
 Best Local Similarity 100.0%; Pred. No. 7.7e-99;
 RESULT 9
 ID ADA06891 standard; protein; 192 AA.
 DE Human PRO polypeptide #24.
 PN US2003068781-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1036; DB 7; Length 192;
 Best Local Similarity 100.0%; Pred. No. 7.7e-99;
 RESULT 10
 ID ADA08379 standard; protein; 192 AA.
 DE Novel human secreted and transmembrane protein PRO4487.
 PN US2003068783-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1036; DB 7; Length 192;
 Best Local Similarity 100.0%; Pred. No. 7.7e-99;
 RESULT 11
 ID AD899672 standard; protein; 192 AA.
 DE Human PRO polypeptide SEQ ID 48.
 PN US2003082728-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1036; DB 7; Length 192;
 Best Local Similarity 100.0%; Pred. No. 7.7e-99;
 RESULT 12
 ID AD886955 standard; protein; 192 AA.
 DE Human PRO polypeptide #24.
 PN US2003082726-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1036; DB 7; Length 192;
 Best Local Similarity 100.0%; Pred. No. 7.7e-99;
 RESULT 13
 ID ADB66110 standard; protein; 192 AA.
 DE Human secreted/transmembrane polypeptide PRO4487.
 PN US2003082729-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1036; DB 7; Length 192;
 Best Local Similarity 100.0%; Pred. No. 7.7e-99;
 RESULT 14
 ID AD899788 standard; protein; 192 AA.
 DE Human PRO polypeptide SEQ ID 48.
 PN US2003073192-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1036; DB 7; Length 192;
 Best Local Similarity 100.0%; Pred. No. 7.7e-99;
 RESULT 15
 ID AD899443 standard; protein; 192 AA.
 DE Novel human secreted and transmembrane protein PRO4487.

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PN US2003082731-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1036; DB 7; Length 192;
RESULT 16
ID AD865994 standard; protein; 192 AA.
DE Human secreted/transmembrane polypeptide PRO4487.
PN US2003082732-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1036; DB 7; Length 192;
RESULT 17
ID ADC23392 standard; protein; 192 AA.
DE Human transmembrane PRO polypeptide (SeqID 48) .
PN US2003073193-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1036; DB 7; Length 192;
RESULT 18
ID ADC26085 standard; protein; 192 AA.
DE Human PRO4487 protein.
PN US2003073194-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1036; DB 7; Length 192;
RESULT 19
ID ADS04912 standard; protein; 192 AA.
DE Human PRO polypeptide #24.
PN US2003068778-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1036; DB 7; Length 192;
RESULT 20
ID ADE11218 standard; protein; 192 AA.
DE Human PRO polypeptide #24.
PN US2003073191-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1036; DB 7; Length 192;
RESULT 21
ID ADD88149 standard; protein; 192 AA.
DE Human PRO polypeptide #24.
PN US2003082733-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1036; DB 7; Length 192;
RESULT 22
ID ADD95444 standard; protein; 192 AA.
DE Human secreted/transmembrane polypeptide PRO4487.
PN US2003064473-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1036; DB 7; Length 192;
RESULT 23
ID ADE06374 standard; protein; 192 AA.
DE Human PRO polypeptide #24.
PN US2003073195-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1036; DB 7; Length 192;
RESULT 24
ID ADE38149 standard; protein; 192 AA.
DE Human PRO polypeptide #24.
PN US2003119120-A1.

PN US2003082731-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1036; DB 7; Length 192;
RESULT 25
ID ADD88265 standard; protein; 192 AA.
DE Human PRO polypeptide #24.
PN US2003073189-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1036; DB 7; Length 192;
RESULT 26
ID ADD90846 standard; protein; 192 AA.
DE Human secreted/transmembrane polypeptide PRO4487.
PN US2003073188-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1036; DB 7; Length 192;
RESULT 27
ID ADF9401 standard; protein; 192 AA.
DE Human secreted/transmembrane polypeptide PRO4487.
PN US2003078401-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1036; DB 7; Length 192;
RESULT 28
ID ADG06494 standard; protein; 192 AA.
DE Human PRO polypeptide #24.
PN US2003077742-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1036; DB 7; Length 192;
RESULT 29
ID ADG05445 standard; protein; 192 AA.
DE Human PRO polypeptide #24.
PN US2003077741-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1036; DB 7; Length 192;
RESULT 30
ID ADG82446 standard; protein; 192 AA.
DE Human PRO polypeptide #24.
PN US2003077744-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1036; DB 7; Length 192;
RESULT 31
ID ADE51699 standard; protein; 192 AA.
DE Human secreted/transmembrane polypeptide PRO4487.
PN US2003104560-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1036; DB 8; Length 192;
RESULT 32
ID ADE51815 standard; protein; 192 AA.
DE Human secreted/transmembrane polypeptide PRO4487.
PN US2003104561-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1036; DB 8; Length 192;
RESULT 33
ID ADE37673 standard; protein; 192 AA.
DE Human secreted/transmembrane polypeptide PRO4487.
PN US2003104564-A1.
PD 05-JUN-2003.
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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 34
ID ADE37557 standard; protein; 192 AA.
DE Human secreted/transmembrane polypeptide PRO4487.
PN US2003104565-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 35
ID ADD95328 standard; protein; 192 AA.
DE Human secreted/transmembrane polypeptide PRO4487.
PN US2003138901-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 36
ID ADE38028 standard; protein; 192 AA.
DE Human PRO polypeptide #24.
PN US2003104566-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 37
ID ADE76117 standard; protein; 192 AA.
DE Human PRO polypeptide #24.
PN US2003124665-A1.
PD 03-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 38
ID ADE39440 standard; protein; 192 AA.
DE Human PRO polypeptide #24.
PN US2003119117-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 39
ID ADE04244 standard; protein; 192 AA.
DE Human PRO polypeptide #24.
PN US2003093634-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 40
ID ADE39841 standard; protein; 192 AA.
DE Human PRO polypeptide #24.
PN US2003138896-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 41
ID ADE19706 standard; protein; 192 AA.
DE Human PRO polypeptide #24.
PN US2003138903-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 42
ID ADE77284 standard; protein; 192 AA.
DE Human secreted/transmembrane polypeptide PRO4487.
PN US2003124666-A1.
PD 03-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 43
ID ADE65392 standard; protein; 192 AA.
DE Human PRO polypeptide #24.
PN US2003119116-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 44
ID ADE76001 standard; protein; 192 AA.
DE Human PRO polypeptide #24.
PN US2003124663-A1.
PD 03-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 45
ID ADE37912 standard; protein; 192 AA.
DE Human PRO polypeptide #24.
PN US2003119119-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 46
ID ADE64522 standard; protein; 192 AA.
DE Human PRO polypeptide #24.
PN US2003119114-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 47
ID ADE38857 standard; protein; 192 AA.
DE Human PRO polypeptide #24.
PN US2003093633-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 48
ID ADE51931 standard; protein; 192 AA.
DE Human secreted/transmembrane polypeptide PRO4487.
PN US2003104562-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 49
ID ADD90962 standard; protein; 192 AA.
DE Human secreted/transmembrane polypeptide PRO4487.
PN US2003138902-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 50
ID ADE38741 standard; protein; 192 AA.
DE Human PRO polypeptide #24.
PN US2003108996-A1.
PD 12-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 51
ID ADE37441 standard; protein; 192 AA.
DE Human secreted/transmembrane polypeptide PRO4487.
PN US2003104563-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
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Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 52
ID ADE06258 standard; protein; 192 AA.
DE Human PRO polypeptide #24.
PN US2003138898-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 53
ID ADP90117 standard; protein; 192 AA.
DE Human secreted/transmembrane polypeptide PRO4487.
PN US2003138904-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 54
ID ADP38625 standard; protein; 192 AA.
DE Human PRO polypeptide #24.
PN US2003119086-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 55
ID ADE39556 standard; protein; 192 AA.
DE Human PRO polypeptide #24.
PN US2003119118-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 56
ID ADP89161 standard; protein; 192 AA.
DE Human PRO polypeptide #24.
PN US2003138897-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 57
ID ADP88928 standard; protein; 192 AA.
DE Human PRO polypeptide #24.
PN US2003138899-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 58
ID ADE19822 standard; protein; 192 AA.
DE Human PRO polypeptide #24.
PN US2003138900-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 59
ID ADE77400 standard; protein; 192 AA.
DE Human secreted/transmembrane polypeptide PRO4487.
PN US2003124667-A1.
PD 03-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 60
ID ADE65276 standard; protein; 192 AA.
DE Human PRO polypeptide #24.
PN US2003119113-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 61
ID ADE39324 standard; protein; 192 AA.
DE Human PRO polypeptide #24.
PN US2003119115-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 62
ID ADE38509 standard; protein; 192 AA.
DE Human secreted/transmembrane polypeptide PRO4487.
PN US2003104559-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 63
ID ADG11062 standard; protein; 192 AA.
DE Human secreted/transmembrane polypeptide PRO4487.
PN US2003170809-A1.
PD 11-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 64
ID ADG10946 standard; protein; 192 AA.
DE Human secreted/transmembrane polypeptide PRO4487.
PN US2003077743-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 65
ID ADH31474 standard; protein; 192 AA.
DE Human PRO polypeptide #24.
PN US2003119139-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 66
ID ADH38722 standard; protein; 192 AA.
DE Human secreted/transmembrane polypeptide PRO4487.
PN US2003119140-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 67
ID ADH29357 standard; protein; 192 AA.
DE Human secreted/transmembrane polypeptide PRO4487.
PN US2003119137-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 68
ID ADH23660 standard; protein; 192 AA.
DE Human secreted/transmembrane polypeptide PRO4487.
PN US2003119143-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 69
ID ADH26990 standard; protein; 192 AA.
DE Human secreted/transmembrane polypeptide PRO4487.
PN US2003119135-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 70
ID ADH23660 standard; protein; 192 AA.
DE Human secreted/transmembrane polypeptide PRO4487.
PN US2003119135-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
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ID ADH38258 standard; protein; 192 AA.
DE Novel human secreted and transmembrane protein PRO4487.
PN US2003119124-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 71
ID ADH26874 standard; protein; 192 AA.
DE Human secreted/transmembrane polypeptide PRO4487.
PN US2003119134-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 72
ID ADH38142 standard; protein; 192 AA.
DE Novel human secreted and transmembrane protein PRO4487.
PN US2003119123-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 73
ID ADH38838 standard; protein; 192 AA.
DE Human secreted/transmembrane polypeptide PRO4487.
PN US2003119141-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 74
ID ADH23776 standard; protein; 192 AA.
DE Human secreted/transmembrane polypeptide PRO4487.
PN US2003119142-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 75
ID ADH40152 standard; protein; 192 AA.
DE Human PRO4487 protein.
PN US2003119132-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 76
ID ADH40036 standard; protein; 192 AA.
DE Human PRO4487 protein.
PN US2003119133-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 77
ID ADH31358 standard; protein; 192 AA.
DE Human PRO polypeptide #24.
PN US2003119138-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 78
ID ADH29236 standard; protein; 192 AA.
DE Human secreted/transmembrane polypeptide PRO4487.
PN US2003119136-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 79
ID ADH49451 standard; protein; 192 AA.
DE Human PRO polypeptide #24.

DE Novel human secreted and transmembrane protein PRO4487.
PN US2003119127-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 80
ID ADH51915 standard; protein; 192 AA.
DE Novel human secreted and transmembrane protein PRO4487.
PN US2003119125-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 81
ID ADH49770 standard; protein; 192 AA.
DE Novel human secreted and transmembrane protein PRO4487.
PN US2003119128-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 82
ID ADH52371 standard; protein; 192 AA.
DE Novel human secreted and transmembrane protein PRO4487.
PN US2003119130-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 83
ID ADH52487 standard; protein; 192 AA.
DE Novel human secreted and transmembrane protein PRO4487.
PN US2003119129-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 84
ID ADH58484 standard; protein; 192 AA.
DE Novel human secreted and transmembrane protein PRO4487.
PN US2003119121-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 85
ID ADH51799 standard; protein; 192 AA.
DE Novel human secreted and transmembrane protein PRO4487.
PN US2003119126-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 86
ID ADH58360 standard; protein; 192 AA.
DE Novel human secreted and transmembrane protein PRO4487.
PN US2003119122-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 87
ID ADH13557 standard; protein; 192 AA.
DE Novel human secreted and transmembrane protein PRO4487.
PN US2003119131-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1036; DB 8; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.7e-99;
RESULT 88
ID ADK00813 standard; protein; 192 AA.
DE Human PRO polypeptide #24.

PN US2003186373-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 1036; DB 8; Length 192;
 RESULT 89
 ID ADL08554 standard; protein; 192 AA.
 DE Human secreted/transmembrane polypeptide PRO4487.
 PN US2003186372-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 1036; DB 8; Length 192;
 RESULT 90
 ID AM41523 standard; protein; 201 AA.
 DE Human polypeptide SEQ ID NO 6454.
 PN WO200153312-A1.
 PD 26-JUL-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match
 Best Local Similarity 100.0%; Score 1036; DB 4; Length 201;
 RESULT 91
 ID AM41522 standard; protein; 201 AA.
 DE Human polypeptide SEQ ID NO 6453.
 PN WO200153312-A1.
 PD 26-JUL-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match
 Best Local Similarity 100.0%; Score 1036; DB 4; Length 201;
 RESULT 92
 ID ADE09229 standard; protein; 201 AA.
 DE Novel protein-related contig polypeptide sequence #295.
 PN WO2003054152-A2.
 PD 03-JUL-2003.
 PA (HYSE-) HYSEQ INC.
 Query Match
 Best Local Similarity 100.0%; Score 1036; DB 7; Length 201;
 RESULT 93
 ID AA87276 standard; protein; 197 AA.
 DE Human signal peptide containing protein HSPP-53 SEQ ID NO:53.
 PN WO200006310-A2.
 PD 06-JAN-2000.
 PA (INCY-) INCYTE PHARM INC.
 Query Match
 Best Local Similarity 99.3%; Score 1029; DB 3; Length 197;
 RESULT 94
 ID ADE08239 standard; protein; 185 AA.
 DE Novel protein (useful for identifying genetic disorders) #394.
 PN WO2003054152-A2.
 PD 03-JUL-2003.
 PA (HYSE-) HYSEQ INC.
 Query Match
 Best Local Similarity 84.5%; Score 875; DB 7; Length 185;
 RESULT 95
 ID AM39737 standard; protein; 185 AA.
 DE Human polypeptide SEQ ID NO 2882.
 PN WO200153312-A1.
 PD 26-JUL-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match
 Best Local Similarity 84.0%; Score 870; DB 4; Length 185;
 RESULT 96
 ID AGI7101 standard; protein; 198 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 17995.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 PA (HYSE-) HYSEQ INC.
 Query Match
 Best Local Similarity 40.8%; Score 423; DB 3; Length 198;
 RESULT 97
 ID AB62503 standard; protein; 166 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 14301.
 PN WO200171042-A2.
 PD 27-SEP-2001.

PA (PEKE) PE CORP NY.
 Query Match
 Best Local Similarity 39.6%; Score 410.5; DB 4; Length 166;
 RESULT 98
 ID ADF07913 standard; protein; 164 AA.
 DE Bacterial polypeptide #4026.
 PN US6605709-B1.
 PD 12-AUG-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match
 Best Local Similarity 39.5%; Score 409.5; DB 7; Length 164;
 RESULT 99
 ID AAG17102 standard; protein; 153 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 17996.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match
 Best Local Similarity 39.4%; Score 408.5; DB 3; Length 153;
 RESULT 100
 ID ABO61311 standard; protein; 155 AA.
 DE Klebsiella pneumoniae polypeptide seqid 7828.
 PN US6610836-B1.
 PD 26-AUG-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match
 Best Local Similarity 49.0%; Score 406.5; DB 7; Length 155;
 RESULT 101
 ID ABO77568 standard; protein; 186 AA.
 DE Pseudomonas aeruginosa polypeptide #9743.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match
 Best Local Similarity 50.3%; Score 406.5; DB 7; Length 186;
 RESULT 102
 ID ABR44257 standard; protein; 214 AA.
 DE O. sativa DNA-binding factor-1 (OsDBF-1) protein.
 PN WO2003040344-A2.
 PD 15-MAY-2003.
 PA (BADI) BASF PLANT SCI GMBH.
 Query Match
 Best Local Similarity 39.0%; Score 404; DB 6; Length 214;
 RESULT 103
 ID ABM69887 standard; protein; 137 AA.
 DE Photorhabdus luminescens protein sequence #2984.
 PN WO200294867-A2.
 PD 28-NOV-2002.
 PA (INSP) INST PASTEUR.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 Query Match
 Best Local Similarity 37.9%; Score 393; DB 6; Length 137;
 RESULT 104
 ID ABR44255 standard; protein; 207 AA.
 DE P. patens DNA-binding factor-3 (DBF-3) protein.
 PN WO2003040344-A2.
 PD 15-MAY-2003.
 PA (BADI) BASF PLANT SCI GMBH.
 Query Match
 Best Local Similarity 53.9%; Score 375; DB 6; Length 207;
 RESULT 105
 ID AAB21041 standard; protein; 182 AA.
 DE Human nucleic acid-binding protein, NuABP-45.
 PN WO200044900-A2.
 PD 03-AUG-2000.
 PA (INCY-) INCYTE PHARM INC.
 Query Match
 Best Local Similarity 34.4%; Score 356; DB 3; Length 182;
 RESULT 106
 ID ABU09036 standard; protein; 182 AA.
 DE Human pilin-like transcription factor PILB.
 PN US2003008301-A1.
 PD 09-JAN-2003.
 PA (SKLA/) SKLAR P.

PA (LAND/) LANDER E S.
PA (SCHW/) SCHWAB S.
PA (WILD/) WILDENAUER D.
Query Match 34.4%; Score 356; DB 6; Length 182;
Best Local Similarity 47.3%; Pred. No. 2.4e-28;
RESULT 107
ID ADJ6866 standard; protein; 182 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID672.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 34.4%; Score 356; DB 7; Length 182;
Best Local Similarity 47.3%; Pred. No. 2.4e-28;
RESULT 108
ID ADJ6938 standard; protein; 201 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1344.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 34.1%; Score 353.5; DB 7; Length 201;
Best Local Similarity 47.6%; Pred. No. 5e-28;
RESULT 109
ID AAB32686 standard; protein; 133 AA.
DE Eucalyptus grandis transcription factor protein sequence #144.
PN WO200053724-A2.
PD 14-SEP-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Query Match 33.6%; Score 348.5; DB 3; Length 133;
Best Local Similarity 52.6%; Pred. No. 9.4e-28;
RESULT 110
ID ADA35619 standard; protein; 143 AA.
DE Acinetobacter baumannii protein #2780.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 33.6%; Score 348; DB 6; Length 143;
Best Local Similarity 49.6%; Pred. No. 1.2e-27;
RESULT 111
ID ABP77145 standard; protein; 532 AA.
DE N. gonorrhoeae amino acid sequence SEQ ID 820.
PN WO200292243-A2.
PD 10-OCT-2002.
PA (CHIR-) CHIRON SPA.
Query Match 32.1%; Score 332.5; DB 6; Length 532;
Best Local Similarity 49.6%; Pred. No. 2.9e-25;
RESULT 112
ID ABP27500 standard; protein; 145 AA.
DE Streptococcus polypeptide SEQ ID NO 4176.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
Query Match 31.3%; Score 324.5; DB 5; Length 145;
Best Local Similarity 50.8%; Pred. No. 3.3e-25;
RESULT 113
ID ADL04935 standard; protein; 138 AA.
DE M. catarrhalis protein #701.
PN US6673910-B1.
PD 06-JAN-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 31.0%; Score 321.5; DB 8; Length 138;
Best Local Similarity 51.7%; Pred. No. 6.2e-25;
RESULT 114
ID AAW98324 standard; protein; 359 AA.
DE H. pylori GHP0 1411 protein.
PN WO9843478-A1.
PD 08-OCT-1998.
PA (INMR-) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 30.9%; Score 320.5; DB 2; Length 359;

Best Local Similarity 46.6%; Pred. No. 2.9e-24;
RESULT 115
ID ABP27499 standard; protein; 144 AA.
DE Streptococcus polypeptide SEQ ID NO 4174.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 30.0%; Score 310.5; DB 5; Length 144;
Best Local Similarity 47.8%; Pred. No. 9.1e-24;
RESULT 116
ID ADB11488 standard; protein; 143 AA.
DE Alloiococcus otitis antigenic protein SEQ ID NO:5572.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Query Match 29.9%; Score 309.5; DB 6; Length 143;
Best Local Similarity 48.1%; Pred. No. 1.1e-23;
RESULT 117
ID AAG52591 standard; protein; 176 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 66872.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 29.8%; Score 308.5; DB 3; Length 176;
Best Local Similarity 42.1%; Pred. No. 1.9e-23;
RESULT 118
ID AAG52590 standard; protein; 184 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 66871.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 29.8%; Score 308.5; DB 3; Length 184;
Best Local Similarity 42.1%; Pred. No. 2.1e-23;
RESULT 119
ID AAG10503 standard; protein; 138 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 8853.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 29.5%; Score 305.5; DB 3; Length 138;
Best Local Similarity 49.2%; Pred. No. 2.8e-23;
RESULT 120
ID AAG46942 standard; protein; 138 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 59110.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 29.5%; Score 305.5; DB 3; Length 138;
Best Local Similarity 49.2%; Pred. No. 2.8e-23;
RESULT 121
ID AAG46941 standard; protein; 202 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 59109.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 29.5%; Score 305.5; DB 3; Length 202;
Best Local Similarity 49.2%; Pred. No. 4.8e-23;
RESULT 122
ID AAG10502 standard; protein; 202 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 8852.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 29.5%; Score 305.5; DB 3; Length 202;
Best Local Similarity 49.2%; Pred. No. 4.8e-23;
RESULT 123
ID ADN74515 standard; protein; 202 AA.
DE Thale cress protein repressed in E2Fa/Dpa expressing plants SeqID 2410.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPPDESIGN NV.
Query Match 29.5%; Score 305.5; DB 8; Length 202;
Best Local Similarity 49.2%; Pred. No. 4.8e-23;
RESULT 124
ID AAG46940 standard; protein; 203 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 59108.
PN EP1033405-A2.
PD 06-SEP-2000.

Query Match 29.5%; Score 305.5; DB 3; Length 203;
Best Local Similarity 49.2%; Pred. No. 4.8e-23;
RESULT 125
ID AAG10501 standard; protein; 204 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 8851.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 29.5%; Score 305.5; DB 3; Length 204;
Best Local Similarity 49.2%; Pred. No. 4.9e-23;
RESULT 126
ID AAG91831 standard; protein; 136 AA.
DE C glutamicum protein fragment SEQ ID NO: 5585.
PN EP1108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 29.3%; Score 304; DB 4; Length 136;
Best Local Similarity 47.2%; Pred. No. 4e-23;
RESULT 127
ID ADI13240 standard; protein; 136 AA.
DE C. glutamicum stability and folding associated protein RXA01710.
PN WO2003040180-A2.
PD 15-MAY-2003.
PA (BADI) BASF AG.
Query Match 29.3%; Score 304; DB 7; Length 136;
Best Local Similarity 47.2%; Pred. No. 4e-23;
RESULT 128
ID ABJ19035 standard; protein; 142 AA.
DE Pathogen specific antigen related staphylococcal protein SEQ ID NO 284.
PN WO200259148-A2.
PD 01-AUG-2002.
PA (CJST-) CJSTEM BIOTECHNOLOGIES GMBH.
Query Match 29.3%; Score 303.5; DB 6; Length 142;
Best Local Similarity 45.5%; Pred. No. 4.8e-23;
RESULT 129
ID ABP38290 standard; protein; 154 AA.
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3135.
PN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 29.3%; Score 303.5; DB 5; Length 154;
Best Local Similarity 45.5%; Pred. No. 5.3e-23;
RESULT 130
ID ADS04740 standard; protein; 154 AA.
DE Staphylococcus epidermis polypeptide seqid 4035.
PN US2004147734-A1.
PD 29-JUL-2004.
PA (DOUC/) DOUCETTE-STAMM L.
PA (BUSH/) BUSH D.
Query Match 29.3%; Score 303.5; DB 8; Length 154;
Best Local Similarity 45.5%; Pred. No. 5.3e-23;
RESULT 131
ID AAU31230 standard; protein; 231 AA.
DE Novel human secreted protein #1721.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HVSE-) HVSEQ INC.
Query Match 29.3%; Score 303.5; DB 4; Length 231;
Best Local Similarity 42.7%; Pred. No. 9.3e-23;
RESULT 132
ID AAW61244 standard; protein; 331 AA.
DE Streptococcus pneumoniae SP120 protein.
PN WO9818930-A2.
PD 07-MAY-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 29.2%; Score 302.5; DB 2; Length 331;
Best Local Similarity 46.8%; Pred. No. 1.9e-22;
RESULT 133
ID ABP54662 standard; protein; 331 AA.
DE S. pneumoniae SP120 protein sequence SEQ ID NO:212.
PN US2002061545-A1.
PD 23-MAY-2002.
PA (CHOI/) CHOI G H.
PA (KUNS/) KUNSCH C A.

PA (BARA/) BARASH S C.
PA (DILL/) DILLON P J.
PA (DOUG/) DOUGHERTY B.
PA (FANN/) FANNON M R.
PA (ROSE/) ROSEN C A.
Query Match 29.2%; Score 302.5; DB 5; Length 331;
Best Local Similarity 46.8%; Pred. No. 1.9e-22;
RESULT 134
ID ADC45293 standard; protein; 331 AA.
DE S. pneumoniae antigenic protein SP120.
PN US6573082-B1.
PD 03-JUN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 29.2%; Score 302.5; DB 7; Length 331;
Best Local Similarity 46.8%; Pred. No. 1.9e-22;
RESULT 135
ID AAM61234 standard; protein; 344 AA.
DE Streptococcus pneumoniae SP109 protein.
PN WO9818930-A2.
PD 07-MAY-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 29.2%; Score 302.5; DB 2; Length 344;
Best Local Similarity 46.8%; Pred. No. 2e-22;
RESULT 136
ID ABP54652 standard; protein; 344 AA.
DE S. pneumoniae SP109 protein sequence SEQ ID NO:192.
PN US2002061545-A1.
PD 23-MAY-2002.
PA (CHOI/) CHOI G H.
PA (KUNS/) KUNSCH C A.
PA (BARA/) BARASH S C.
PA (DILL/) DILLON P J.
PA (DOUG/) DOUGHERTY B.
PA (FANN/) FANNON M R.
PA (ROSE/) ROSEN C A.
Query Match 29.2%; Score 302.5; DB 5; Length 344;
Best Local Similarity 46.8%; Pred. No. 2e-22;
RESULT 137
ID ADC45273 standard; protein; 344 AA.
DE S. pneumoniae antigenic protein SP109.
PN US6573082-B1.
PD 03-JUN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 29.2%; Score 302.5; DB 7; Length 344;
Best Local Similarity 46.8%; Pred. No. 2e-22;
RESULT 138
ID ABU01042 standard; protein; 370 AA.
DE S. pneumoniae type 4 strain protein from coding region #613.
PN WO200277021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 29.2%; Score 302.5; DB 6; Length 370;
Best Local Similarity 46.8%; Pred. No. 2.2e-22;
RESULT 139
ID ADK48736 standard; protein; 370 AA.
DE Streptococcus pneumoniae protein, Seq ID No 5251.
PN US6699703-B1.
PD 02-MAR-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 29.2%; Score 302.5; DB 8; Length 370;
Best Local Similarity 46.8%; Pred. No. 2.2e-22;
RESULT 140
ID AAY81672 standard; protein; 371 AA.
DE Streptococcus pneumoniae protein sequence ID209 - 4126.3.
PN WO200006737-A2.
PD 10-FEB-2000.
PA (MFCR-) MICROBIAL TECHNIQS LTD.
Query Match 29.2%; Score 302.5; DB 3; Length 371;
Best Local Similarity 46.8%; Pred. No. 2.3e-22;
RESULT 141
ID ADR95486 standard; protein; 375 AA.
DE Novel S. pneumoniae protein sequence, SEQ ID 4121.

PN US6800744-B1.
PD 05-OCT-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 29.2%; Score 302.5; DB 8; Length 375;
Best Local Similarity 46.8%; Pred. No. 2.3e-22;
RESULT 142
ID ABR44258 standard; protein; 204 AA.
DE O. sativa DNA-binding factor-2 (OSDBF-2) protein.
PN WO2003040344-A2.
PD 15-MAY-2003.
PA (BADI) BASF PLANT SCI GMBH.
Query Match 29.1%; Score 301; DB 6; Length 204;
Best Local Similarity 39.3%; Pred. No. 1.4e-22;
RESULT 143
ID AAG34190 standard; protein; 207 AA.
DE Zea mays protein fragment SEQ ID NO: 41561.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 29.0%; Score 300.5; DB 3; Length 207;
Best Local Similarity 38.3%; Pred. No. 1.6e-22;
RESULT 144
ID AAG34189 standard; protein; 217 AA.
DE Zea mays protein fragment SEQ ID NO: 41560.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 29.0%; Score 300.5; DB 3; Length 217;
Best Local Similarity 38.3%; Pred. No. 1.7e-22;
RESULT 145
ID AAG34188 standard; protein; 223 AA.
DE Zea mays protein fragment SEQ ID NO: 41559.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 29.0%; Score 300.5; DB 3; Length 223;
Best Local Similarity 38.3%; Pred. No. 1.8e-22;
RESULT 146
ID AAG30479 standard; protein; 281 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36446.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 29.0%; Score 300; DB 3; Length 281;
Best Local Similarity 38.9%; Pred. No. 2.8e-22;
RESULT 147
ID AAG52589 standard; protein; 282 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 66869.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 28.9%; Score 299.5; DB 3; Length 282;
Best Local Similarity 38.7%; Pred. No. 3.2e-22;
RESULT 148
ID AAG20065 standard; protein; 136 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 22107.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 28.8%; Score 298; DB 3; Length 136;
Best Local Similarity 42.7%; Pred. No. 1.7e-22;
RESULT 149
ID AAG52592 standard; protein; 136 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 66873.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 28.8%; Score 298; DB 3; Length 136;
Best Local Similarity 42.7%; Pred. No. 1.7e-22;
RESULT 150
ID AAG21146 standard; protein; 172 AA.
DE Zea mays protein fragment SEQ ID NO: 23595.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 28.7%; Score 297; DB 3; Length 172;
Best Local Similarity 39.6%; Pred. No. 2.9e-22;
RESULT 151
ID ABR44256 standard; protein; 212 AA.
DE B. napus DNA-binding factor-1 (BnDBF-1) protein.
PN WO2003040344-A2.

PD 15-MAY-2003.
PA (BADI) BASF PLANT SCI GMBH.
Query Match 28.6%; Score 296.5; DB 6; Length 212;
Best Local Similarity 46.0%; Pred. No. 4.4e-22;
RESULT 152
ID AAG46938 standard; protein; 175 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 59105.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 28.5%; Score 295; DB 3; Length 175;
Best Local Similarity 41.1%; Pred. No. 4.8e-22;
RESULT 153
ID AAG09088 standard; protein; 176 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 6882.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 28.4%; Score 294; DB 3; Length 176;
Best Local Similarity 41.1%; Pred. No. 6.2e-22;
RESULT 154
ID ADM46982 standard; protein; 340 AA.
DE Thermococcus kodakaraensis KOD1 protein sequence SeqID860.
PN WO2004022736-A1.
PD 18-MAR-2004.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 28.3%; Score 293.5; DB 8; Length 340;
Best Local Similarity 48.8%; Pred. No. 1.7e-21;
RESULT 155
ID AAG09089 standard; protein; 143 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 6883.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 28.2%; Score 292; DB 3; Length 143;
Best Local Similarity 43.7%; Pred. No. 7.5e-22;
RESULT 156
ID AAG46939 standard; protein; 143 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 59106.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 28.2%; Score 292; DB 3; Length 143;
Best Local Similarity 43.7%; Pred. No. 7.5e-22;
RESULT 157
ID ABB49390 standard; protein; 145 AA.
DE Listeria monocytogenes protein #2094.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 27.9%; Score 289.5; DB 5; Length 145;
Best Local Similarity 44.0%; Pred. No. 1.4e-21;
RESULT 158
ID ABW73024 standard; protein; 142 AA.
DE Staphylococcus aureus protein #2264.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 27.8%; Score 287.5; DB 6; Length 142;
Best Local Similarity 47.9%; Pred. No. 2.2e-21;
RESULT 159
ID ADL04406 standard; protein; 579 AA.
DE M. catarrhalis protein #172.
PN US6673910-B1.
PD 06-JAN-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 27.8%; Score 287.5; DB 8; Length 579;
Best Local Similarity 44.1%; Pred. No. 1.5e-20;
RESULT 160
ID AAU62755 standard; protein; 172 AA.
DE Propionibacterium acnes immunogenic protein #23651.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 27.6%; Score 285.5; DB 4; Length 172;
Best Local Similarity 40.6%; Pred. No. 4.6e-21;
RESULT 161

ID ABM59274 standard; protein; 172 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #23950.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 27.6%; Score 285.5; DB 6; Length 172;
Best Local Similarity 40.6%; Pred. No. 4.6e-21;
RESULT 162
ID ADK47052 standard; protein; 255 AA.
DE Streptococcus pneumoniae protein, Seq ID No 3567.
PN US6699703-B1.
PD 02-MAR-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 27.6%; Score 285.5; DB 8; Length 255;
Best Local Similarity 45.0%; Pred. No. 7.8e-21;
RESULT 163
ID ADR95700 standard; protein; 257 AA.
DE Novel S. pneumoniae protein sequence, SEQ ID 4335.
PN US6800744-B1.
PD 05-OCT-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 27.6%; Score 285.5; DB 8; Length 257;
Best Local Similarity 45.0%; Pred. No. 7.9e-21;
RESULT 164
ID AAW69788 standard; protein; 312 AA.
DE Streptococcus pneumoniae peptide methionine sulfoxide reductase.
PN US5798243-A.
PD 25-AUG-1998.
PA (UVRQ) UNIV ROCKEFELLER.
Query Match 27.6%; Score 285.5; DB 2; Length 312;
Best Local Similarity 45.0%; Pred. No. 1e-20;
RESULT 165
ID AAW68553 standard; protein; 312 AA.
DE S. pneumoniae peptide methionine sulphoxide reductase.
PN US5834278-A.
PD 10-NOV-1998.
PA (UVRQ) UNIV ROCKEFELLER.
Query Match 27.6%; Score 285.5; DB 2; Length 312;
Best Local Similarity 45.0%; Pred. No. 1e-20;
RESULT 166
ID AAY81773 standard; protein; 312 AA.
DE Streptococcus pneumoniae protein sequence ID15.
PN WO300006738-A2.
PD 10-FEB-2000.
PA (MICR-) MICROBIAL TECHNIQS LTD.
Query Match 27.6%; Score 285.5; DB 3; Length 312;
Best Local Similarity 45.0%; Pred. No. 1e-20;
RESULT 167
ID ABU01800 standard; protein; 312 AA.
DE S. pneumoniae type 4 strain protein from coding region #1376.
PN WO200277021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 27.6%; Score 285.5; DB 6; Length 312;
Best Local Similarity 45.0%; Pred. No. 1e-20;
RESULT 168
ID ABP30014 standard; protein; 368 AA.
DE Streptococcus polypeptide SEQ ID NO 9204.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 27.5%; Score 285; DB 5; Length 368;
Best Local Similarity 43.3%; Pred. No. 1.5e-20;
RESULT 169
ID AAG21147 standard; protein; 135 AA.
DE Zea mays protein fragment SEQ ID NO: 23596.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 27.5%; Score 284.5; DB 3; Length 135;
Best Local Similarity 44.5%; Pred. No. 4.2e-21;
RESULT 170

ID AAG10971 standard; protein; 141 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 9508.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 27.5%; Score 284.5; DB 3; Length 141;
Best Local Similarity 42.4%; Pred. No. 4.4e-21;
RESULT 171
ID AAG43697 standard; protein; 141 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 54647.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 27.5%; Score 284.5; DB 3; Length 141;
Best Local Similarity 42.4%; Pred. No. 4.4e-21;
RESULT 172
ID AAG46977 standard; protein; 141 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 59158.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 27.5%; Score 284.5; DB 3; Length 141;
Best Local Similarity 42.4%; Pred. No. 4.4e-21;
RESULT 173
ID AAG10970 standard; protein; 143 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 9507.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 27.5%; Score 284.5; DB 3; Length 143;
Best Local Similarity 42.4%; Pred. No. 4.5e-21;
RESULT 174
ID AAG43696 standard; protein; 143 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 54646.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 27.5%; Score 284.5; DB 3; Length 143;
Best Local Similarity 42.4%; Pred. No. 4.5e-21;
RESULT 175
ID AAG46976 standard; protein; 143 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 59157.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 27.5%; Score 284.5; DB 3; Length 143;
Best Local Similarity 42.4%; Pred. No. 4.5e-21;
RESULT 176
ID ADN72731 standard; protein; 143 AA.
DE Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 626.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDESIGN NV.
Query Match 27.5%; Score 284.5; DB 8; Length 143;
Best Local Similarity 42.4%; Pred. No. 4.5e-21;
RESULT 177
ID AAG43242 standard; protein; 139 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 54026.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 27.2%; Score 281.5; DB 3; Length 139;
Best Local Similarity 44.2%; Pred. No. 8.9e-21;
RESULT 178
ID AAG17869 standard; protein; 139 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 19055.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 27.2%; Score 281.5; DB 3; Length 139;
Best Local Similarity 44.2%; Pred. No. 8.9e-21;
RESULT 179
ID AAG46937 standard; protein; 141 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 59103.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 26.9%; Score 278.5; DB 3; Length 141;
Best Local Similarity 41.7%; Pred. No. 1.9e-20;
RESULT 180
ID AAG46936 standard; protein; 143 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 59102.

PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 26.9%; Score 278.5; DB 3; Length 143;
Best Local Similarity 41.7%; Pred. No. 1.9e-20;
RESULT 181
ID ADN74613 standard; protein; 153 AA.
DE Thale cress protein repressed in E2Fa/Dpa expressing plants SeqID 2508.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDESIGN NV.
Query Match 26.9%; Score 278.5; DB 8; Length 153;
Best Local Similarity 45.7%; Pred. No. 2.1e-20;
RESULT 182
ID AAG14999 standard; protein; 141 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 15074.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 26.5%; Score 274.5; DB 3; Length 141;
Best Local Similarity 44.9%; Pred. No. 4.8e-20;
RESULT 183
ID AAG46972 standard; protein; 141 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 59151.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 26.5%; Score 274.5; DB 3; Length 141;
Best Local Similarity 44.9%; Pred. No. 4.8e-20;
RESULT 184
ID AAG14998 standard; protein; 144 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 15073.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 26.5%; Score 274.5; DB 3; Length 144;
Best Local Similarity 44.9%; Pred. No. 5e-20;
RESULT 185
ID AAG46971 standard; protein; 144 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 59150.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 26.5%; Score 274.5; DB 3; Length 144;
Best Local Similarity 44.9%; Pred. No. 5e-20;
RESULT 186
ID ABBS3493 standard; protein; 142 AA.
DE Lactococcus lactis protein ybJA.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 26.4%; Score 273; DB 5; Length 142;
Best Local Similarity 45.5%; Pred. No. 6.9e-20;
RESULT 187
ID AAB37401 standard; protein; 100 AA.
DE Human secreted protein BLAST search protein SEQ ID NO: 111.
PN WO200058335-A1.
PD 05-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 26.3%; Score 272; DB 3; Length 100;
Best Local Similarity 51.0%; Pred. No. 5.5e-20;
RESULT 188
ID AAG27248 standard; protein; 144 AA.
DE Zea mays protein fragment SEQ ID NO: 32011.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 26.0%; Score 269; DB 3; Length 144;
Best Local Similarity 39.9%; Pred. No. 1.8e-19;
RESULT 189
ID ABP65597 standard; protein; 327 AA.
DE Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:341.
PN EP1227152-A1.
PD 31-JUL-2002.
PA (NEST) SOC PROD NESTLE SA.
Query Match 25.9%; Score 268; DB 5; Length 327;
Best Local Similarity 47.3%; Pred. No. 7.2e-19;
RESULT 190

ID AAW89960 standard; protein; 309 AA.
DE Antigen from cluster 59.
PN WO9849314-A2.
PD 05-NOV-1998.
PA (GENE-) GENELABS TECHNOLOGIES INC.
Query Match 25.0%; Score 259; DB 2; Length 309;
Best Local Similarity 43.4%; Pred. No. 5.7e-18;
RESULT 191
ID AAG27250 standard; protein; 127 AA.
DE Zea mays protein fragment SEQ ID NO: 32013.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 25.0%; Score 258.5; DB 3; Length 127;
Best Local Similarity 44.2%; Pred. No. 1.9e-18;
RESULT 192
ID AAG31428 standard; protein; 124 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 37739.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 20.7%; Score 214; DB 3; Length 124;
Best Local Similarity 49.0%; Pred. No. 7.6e-14;
RESULT 193
ID ADG87551 standard; protein; 124 AA.
DE A. thaliana ERF-regulated gene-encoded protein #789.
PN WO200222675-A2.
PD 21-MAR-2002.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
PA (UNNC-) UNIV NORTH CAROLINA.
PA (GLAZ/) GLAZEBROOK J.
PA (WANG/) WANG X.
PA (DANG/) DANG J L.
PA (EULG/) EULGEM T.
PA (ZHUT/) ZHU T.
Query Match 20.7%; Score 214; DB 5; Length 124;
Best Local Similarity 49.0%; Pred. No. 7.6e-14;
RESULT 194
ID AAU31229 standard; protein; 203 AA.
DE Novel human secreted protein #1720.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 19.7%; Score 204.5; DB 4; Length 203;
Best Local Similarity 42.1%; Pred. No. 1.4e-12;
RESULT 195
ID ABUS0789 standard; protein; 108 AA.
DE Helicobacter pylori selected interacting domain (SID) protein #132.
PN WO200266501-A2.
PD 29-AUG-2002.
PA (HYBR-) HYBRIGENICS.
PA (INSP) INST PASTEUR.
Query Match 19.5%; Score 202.5; DB 5; Length 108;
Best Local Similarity 51.9%; Pred. No. 9.8e-13;
RESULT 196
ID ABUS1286 standard; protein; 108 AA.
DE Helicobacter pylori selected interacting domain (SID) protein #630.
PN WO200266501-A2.
PD 29-AUG-2002.
PA (HYBR-) HYBRIGENICS.
PA (INSP) INST PASTEUR.
Query Match 19.5%; Score 202.5; DB 5; Length 108;
Best Local Similarity 51.9%; Pred. No. 9.8e-13;
RESULT 197
ID ABUS1569 standard; protein; 104 AA.
DE Helicobacter pylori selected interacting domain (SID) protein #913.
PN WO200266501-A2.
PD 29-AUG-2002.
PA (HYBR-) HYBRIGENICS.
PA (INSP) INST PASTEUR.
Query Match 18.4%; Score 190.5; DB 5; Length 104;
Best Local Similarity 52.1%; Pred. No. 1.6e-11;
RESULT 198
ID AAB37402 standard; protein; 99 AA.
DE Human secreted protein BLAST search protein SEQ ID NO: 112.

PN WO200058335-A1.
PD 05-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 18.2%; Score 188.5; DB 3; Length 99;
Best Local Similarity 37.0%; Pred. No. 2.5e-11;
RESULT 199
ID ADH87540 standard; protein; 115 AA.
DE Enterococcus faecalis polypeptide #2020.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 16.5%; Score 171; DB 7; Length 115;
Best Local Similarity 51.6%; Pred. No. 2e-09;
RESULT 200
ID ABP64784 standard; protein; 94 AA.
DE Human protein SEQ ID 444.
PN WO200259260-A2.
PD 01-AUG-2002.
PA (HYSE-) HYSEQ INC.
Query Match 16.4%; Score 169.5; DB 5; Length 94;
Best Local Similarity 36.3%; Pred. No. 2.1e-09;
RESULT 201
ID AAY60509 standard; protein; 138 AA.
DE Human normal bladder tissue EST encoded protein 181.
PN DE19818620-A1.
PD 28-OCT-1999.
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
Query Match 16.4%; Score 169.5; DB 2; Length 138;
Best Local Similarity 36.3%; Pred. No. 3.6e-09;
RESULT 202
ID AAW46757 standard; peptide; 83 AA.
DE Exon trap L48792.
PN WO9748797-A1.
PD 24-DEC-1997.
PA (GENZ) GENZYME CORP.
Query Match 15.7%; Score 163; DB 2; Length 83;
Best Local Similarity 34.5%; Pred. No. 8.5e-09;
RESULT 203
ID AAR70154 standard; protein; 173 AA.
DE Streptococcus pneumoniae strain SPRU40 Exp3.
PN WO9506732-A2.
PD 09-MAR-1995.
PA (UVRQ) UNIV ROCKEFELLER.
Query Match 14.8%; Score 153; DB 2; Length 173;
Best Local Similarity 42.3%; Pred. No. 2.5e-07;
RESULT 204
ID ABO14764 standard; protein; 115 AA.
DE Novel human protein #137.
PN WO2003023002-A2.
PD 20-MAR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 14.2%; Score 147; DB 6; Length 115;
Best Local Similarity 33.0%; Pred. No. 6.1e-07;
RESULT 205
ID AAU31228 standard; protein; 53 AA.
DE Novel human secreted protein #1719.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.7%; Score 142; DB 4; Length 53;
Best Local Similarity 54.3%; Pred. No. 7e-07;
RESULT 206
ID ABP07856 standard; protein; 59 AA.
DE Human ORFX protein sequence SEQ ID NO:15694.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match 13.0%; Score 135; DB 5; Length 59;
Best Local Similarity 59.6%; Pred. No. 4.3e-06;
RESULT 207
ID AAY11309 standard; protein; 60 AA.
DE S. pneumoniae PILB protein.
PN WO9737028-A1.
PD 09-OCT-1997.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 11.6%; Score 120.5; DB 2; Length 60;
Best Local Similarity 48.3%; Pred. No. 0.00014;
RESULT 208
ID AAG44103 standard; protein; 45 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 55201.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 10.1%; Score 105; DB 3; Length 45;
Best Local Similarity 43.2%; Pred. No. 0.0038;
RESULT 209
ID AAG46955 standard; protein; 45 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 59128.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 10.1%; Score 105; DB 3; Length 45;
Best Local Similarity 43.2%; Pred. No. 0.0038;
RESULT 210
ID ADN99394 standard; protein; 77 AA.
DE Novel human protein sequence #210.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIMS THERAPEUTICS INC.
Query Match 9.8%; Score 101.5; DB 8; Length 77;
Best Local Similarity 37.3%; Pred. No. 0.018;
RESULT 211
ID ABP09894 standard; protein; 101 AA.
DE Human ORFX protein sequence SEQ ID NO:19770.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match 9.7%; Score 101; DB 5; Length 101;
Best Local Similarity 34.4%; Pred. No. 0.03;
RESULT 212
ID AAG18713 standard; protein; 59 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 20232.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 9.6%; Score 99; DB 3; Length 59;
Best Local Similarity 38.3%; Pred. No. 0.023;
RESULT 213
ID ABP97377 standard; protein; 1207 AA.
DE Human kielin-like protein NHP10, SEQ ID NO:20.
PN WO2003004609-A2.
PD 16-JAN-2003.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 9.3%; Score 96; DB 6; Length 1207;
Best Local Similarity 24.6%; Pred. No. 3;
RESULT 214
ID AAG60258 standard; protein; 148 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 78030.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 8.8%; Score 91.5; DB 3; Length 148;
Best Local Similarity 23.9%; Pred. No. 0.49;
RESULT 215
ID AAG60259 standard; protein; 127 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 78031.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 8.7%; Score 90.5; DB 3; Length 127;
Best Local Similarity 26.4%; Pred. No. 0.51;
RESULT 216
ID AAG58225 standard; protein; 127 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 75135.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 8.7%; Score 90.5; DB 3; Length 127;
Best Local Similarity 26.4%; Pred. No. 0.51;

RESULT 217
ID AAG58224 standard; protein; 149 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 75134.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 8.7%; Score 90.5; DB 3; Length 149;
Best Local Similarity 26.4%; Pred. No. 0.63;
RESULT 218
ID ADC27568 standard; protein; 862 AA.
DE Human colon specific protein (CSP) Seq ID127.
PN WO2003020953-A2.
PD 13-MAR-2003.
PA (DIAD-) DIADEXUS INC.
Query Match 8.6%; Score 89.5; DB 7; Length 862;
Best Local Similarity 28.0%; Pred. No. 8.8;
RESULT 219
ID ABB64450 standard; protein; 2165 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 20142.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 8.6%; Score 89; DB 4; Length 2165;
Best Local Similarity 32.9%; Pred. No. 35;
RESULT 220
ID AAG54394 standard; protein; 98 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 69351.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 8.5%; Score 88.5; DB 3; Length 98;
Best Local Similarity 33.3%; Pred. No. 0.57;
RESULT 221
ID AAG54393 standard; protein; 112 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 69350.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 8.5%; Score 88.5; DB 3; Length 112;
Best Local Similarity 33.3%; Pred. No. 0.69;
RESULT 222
ID ABB67109 standard; protein; 497 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 28119.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 8.2%; Score 84.5; DB 4; Length 497;
Best Local Similarity 25.0%; Pred. No. 14;
RESULT 223
ID ABU11608 standard; protein; 409 AA.
DE Human MDDT polypeptide SEQ ID 555.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 8.1%; Score 84; DB 6; Length 409;
Best Local Similarity 26.7%; Pred. No. 12;
RESULT 224
ID AAG75526 standard; protein; 235 AA.
DE Human colon cancer antigen protein SEQ ID NO:6290.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.0%; Score 82.5; DB 4; Length 235;
Best Local Similarity 28.1%; Pred. No. 7.9;
RESULT 225
ID ABP97375 standard; protein; 1251 AA.
DE Human kielin-like protein NHP8, SEQ ID NO:16.
PN WO2003004609-A2.
PD 16-JAN-2003.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 8.0%; Score 82.5; DB 6; Length 1251;
Best Local Similarity 25.0%; Pred. No. 78;
RESULT 226
ID AAO16437 standard; protein; 388 AA.
DE Human nucleic acid-associated protein (NAAP) - SEQ ID NO 34.
PN WO2003000864-A2.

PD 03-JAN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 7.9%; Score 82; DB 6; Length 388;
Best Local Similarity 26.7%; Pred. No. 18;
RESULT 227
ID AAW94474 standard; protein; 411 AA.
DE Human Ihh hedgehog protein sequence.
PN WO9900117-A2.
PD 07-JAN-1999.
PA (ONTO-) ONTOGENY INC.
Query Match 7.9%; Score 82; DB 2; Length 411;
Best Local Similarity 22.4%; Pred. No. 19;
RESULT 228
ID AAY05860 standard; protein; 411 AA.
DE Human Indian hedgehog Ihh protein.
PN WO9920298-A1.
PD 29-APR-1999.
PA (ONTO-) ONTOGENY INC.
Query Match 7.9%; Score 82; DB 2; Length 411;
Best Local Similarity 22.4%; Pred. No. 19;
RESULT 229
ID AAW97763 standard; protein; 411 AA.
DE Human Indian hedgehog (Ihh) protein.
PN WO9904775-A2.
PD 04-FEB-1999.
PA (ONTO-) ONTOGENY INC.
Query Match 7.9%; Score 82; DB 2; Length 411;
Best Local Similarity 22.4%; Pred. No. 19;
RESULT 230
ID AAY05516 standard; protein; 411 AA.
DE Human Indian hedgehog protein Ihh.
PN WO9910004-A2.
PD 04-MAR-1999.
PA (ONTO-) ONTOGENY INC.
Query Match 7.9%; Score 82; DB 2; Length 411;
Best Local Similarity 22.4%; Pred. No. 19;
RESULT 231
ID AAY96249 standard; protein; 411 AA.
DE Human Ihh.
PN WO200027422-A2.
PD 18-MAY-2000.
PA (BIOJ) BIOGEN INC.
PA (ONTO-) ONTOGENY INC.
Query Match 7.9%; Score 82; DB 3; Length 411;
Best Local Similarity 22.4%; Pred. No. 19;
RESULT 232
ID AAY70682 standard; protein; 411 AA.
DE Human Indian hedgehog (ihh) protein.
PN WO200015246-A2.
PD 23-MAR-2000.
PA (HARD) HARVARD COLLEGE.
Query Match 7.9%; Score 82; DB 3; Length 411;
Best Local Similarity 22.4%; Pred. No. 19;
RESULT 233
ID AAY95287 standard; protein; 411 AA.
DE Human Indian hedgehog Ihh protein.
PN WO200035948-A1.
PD 22-JUN-2000.
PA (BIOJ) BIOGEN INC.
PA (ONTO-) ONTOGENY INC.
Query Match 7.9%; Score 82; DB 3; Length 411;
Best Local Similarity 22.4%; Pred. No. 19;
RESULT 234
ID AAY95978 standard; protein; 411 AA.
DE Human Indian hedgehog ihh protein.
PN WO200051628-A2.
PD 08-SEP-2000.
PA (BIOJ) BIOGEN INC.
Query Match 7.9%; Score 82; DB 3; Length 411;
Best Local Similarity 22.4%; Pred. No. 19;
RESULT 235
ID AAB84675 standard; protein; 411 AA.
DE Amino acid sequence of a human hedgehog (Ihh) polypeptide.

PN WO200140438-A2.
PD 07-JUN-2001.
PA (CURI-) CURIS INC.
Query Match 7.9%; Score 82; DB 4; Length 411;
Best Local Similarity 22.4%; Pred. No. 19;
RESULT 236
ID AAB60266 standard; protein; 411 AA.
DE Human Indian hedgehog (Ihh) protein, SEQ ID NO:16.
PD 07-DEC-2000.
PA (BIOJ) BIOGEN INC.
Query Match 7.9%; Score 82; DB 4; Length 411;
Best Local Similarity 22.4%; Pred. No. 19;
RESULT 237
ID AAE04688 standard; protein; 411 AA.
DE Human Indian hedgehog (Ihh) protein.
PD 17-MAY-2001.
PA (BIOJ) BIOGEN INC.
Query Match 7.9%; Score 82; DB 4; Length 411;
Best Local Similarity 22.4%; Pred. No. 19;
RESULT 238
ID AAB85091 standard; protein; 411 AA.
DE Human Indian hedgehog (Ihh) polypeptide.
PD 14-JUN-2001.
PA (GHO) GEN HOSPITAL CORP.
Query Match 7.9%; Score 82; DB 4; Length 411;
Best Local Similarity 22.4%; Pred. No. 19;
RESULT 239
ID AAG65749 standard; protein; 411 AA.
DE Human Indian hedgehog (Ihh) polypeptide.
PD 07-SEP-2001.
PA (CURI-) CURIS INC.
Query Match 7.9%; Score 82; DB 4; Length 411;
Best Local Similarity 22.4%; Pred. No. 19;
RESULT 240
ID AAE14298 standard; protein; 411 AA.
DE Human Indian hedgehog (Ihh) protein.
PD 08-NOV-2001.
PA (CURI-) CURIS INC.
Query Match 7.9%; Score 82; DB 5; Length 411;
Best Local Similarity 22.4%; Pred. No. 19;
RESULT 241
ID AAO20924 standard; protein; 411 AA.
DE Human Ihh protein sequence SEQ ID NO 16.
PD 27-DEC-2001.
PA (BIOJ) BIOGEN INC.
Query Match 7.9%; Score 82; DB 5; Length 411;
Best Local Similarity 22.4%; Pred. No. 19;
RESULT 242
ID AAU99484 standard; protein; 411 AA.
DE Human Indian hedgehog (Ihh) protein.
PD 06-JUN-2002.
PA (CURI-) CURIS INC.
Query Match 7.9%; Score 82; DB 5; Length 411;
Best Local Similarity 22.4%; Pred. No. 19;
RESULT 243
ID ADK66382 standard; protein; 411 AA.
DE Human Indian hedgehog protein.
PD 26-JUN-2003.
PA (MIAO/) MIAO N.
PA (WANG/) WANG M.
PA (MAHA/) MAHANTHAPPA N K.
PA (JINP/) JIN P.
PA (PANG/) PANG K.
Query Match 7.9%; Score 82; DB 7; Length 411;
Best Local Similarity 22.4%; Pred. No. 19;
RESULT 244
ID ADL06710 standard; protein; 411 AA.
DE Human brachydactyly-body height associated protein #1.
PD 10-APR-2002.
PA (UYSH-) UNIV SHANGHAI JIAOTONG.
Query Match 7.9%; Score 82; DB 7; Length 411;
Best Local Similarity 22.4%; Pred. No. 19;
RESULT 245
ID ADL06712 standard; protein; 411 AA.
DE Human brachydactyly-body height associated protein #2.
PD 10-APR-2002.
PA (UYSH-) UNIV SHANGHAI JIAOTONG.
Query Match 7.9%; Score 82; DB 7; Length 411;
Best Local Similarity 22.4%; Pred. No. 19;
RESULT 246
ID ADH56644 standard; protein; 411 AA.
DE Human Indian hedgehog protein sequence SeqID 16.
PD 27-NOV-2003.
PA (WARZ/) WARZECHA J.
Query Match 7.9%; Score 82; DB 8; Length 411;
Best Local Similarity 22.4%; Pred. No. 19;
RESULT 247
ID ADK82143 standard; protein; 411 AA.
DE Human India hedgehog (Ihh) protein.
PD 11-MAR-2004.
PA (CURI-) CURIS INC.
Query Match 7.9%; Score 82; DB 8; Length 411;
Best Local Similarity 22.4%; Pred. No. 19;
RESULT 248
ID ADR03323 standard; protein; 411 AA.
DE Human Indian hedgehog (Ihh) protein.
PD 27-JUL-2004.
PA (CURI-) CURIS INC.
Query Match 7.9%; Score 82; DB 8; Length 411;
Best Local Similarity 22.4%; Pred. No. 19;
RESULT 249
ID ADM87350 standard; protein; 424 AA.
DE Human protein SEQ ID NO:443.
PD 29-JAN-2004.
PA (NUVE-) NUVELO INC.
Query Match 7.9%; Score 82; DB 8; Length 424;
Best Local Similarity 26.7%; Pred. No. 20;
RESULT 250
ID ABB71557 standard; protein; 697 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 41463.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.9%; Score 81.5; DB 4; Length 697;
Best Local Similarity 21.8%; Pred. No. 45;
RESULT 251
ID ADSI211 standard; protein; 252 AA.
DE Human therapeutic contig protein - SEQ ID 2448.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 7.8%; Score 81; DB 8; Length 252;
Best Local Similarity 23.8%; Pred. No. 12;
RESULT 252
ID AAM93114 standard; protein; 270 AA.
DE Human digestive system antigen SEQ ID NO: 2463.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.8%; Score 80.5; DB 4; Length 270;
Best Local Similarity 28.1%; Pred. No. 15;
RESULT 253

ID AAM38630 standard; protein; 270 AA.
DE Human colorectal cancer antigen SEQ ID NO: 145.
PN WO200155350-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.8%; Score 80.5; DB 4; Length 270;
Best Local Similarity 28.1%; Pred. No. 15;
RESULT 254
ID AAM99931 standard; protein; 270 AA.
DE Human polypeptide SEQ ID NO 47.
PN WO200155173-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.8%; Score 80.5; DB 4; Length 270;
Best Local Similarity 28.1%; Pred. No. 15;
RESULT 255
ID ABG97682 standard; protein; 270 AA.
DE Human colorectal cancer related protein #62.
PN US2002119919-A1.
PD 29-AUG-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 7.8%; Score 80.5; DB 5; Length 270;
Best Local Similarity 28.1%; Pred. No. 15;
RESULT 256
ID ADB92938 standard; protein; 270 AA.
DE Human colorectal cancer related polypeptide #62.
PN US2003054420-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.8%; Score 80.5; DB 7; Length 270;
Best Local Similarity 28.1%; Pred. No. 15;
RESULT 257
ID AAM99918 standard; protein; 361 AA.
DE Human polypeptide SEQ ID NO 34.
PN WO200155173-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.8%; Score 80.5; DB 4; Length 361;
Best Local Similarity 28.1%; Pred. No. 23;
RESULT 258
ID ADQ65592 standard; protein; 814 AA.
DE Novel human protein sequence #565.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 7.8%; Score 80.5; DB 8; Length 814;
Best Local Similarity 28.1%; Pred. No. 70;
RESULT 259
ID ABP97376 standard; protein; 1192 AA.
DE Human kielin-like protein NHP9, SEQ ID NO:18.
PN WO2003004609-A2.
PD 16-JAN-2003.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 7.8%; Score 80.5; DB 6; Length 1192;
Best Local Similarity 28.1%; Pred. No. 1.2e+02;
RESULT 260
ID ABP97379 standard; protein; 1342 AA.
DE Human kielin-like protein NHP12, SEQ ID NO:24.
PN WO2003004609-A2.
PD 16-JAN-2003.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 7.8%; Score 80.5; DB 6; Length 1342;
Best Local Similarity 28.1%; Pred. No. 1.4e+02;
RESULT 261
ID ABP97371 standard; protein; 1477 AA.
DE Human kielin-like protein NHP4, SEQ ID NO:8.
PN WO2003004609-A2.
PD 16-JAN-2003.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 7.8%; Score 80.5; DB 6; Length 1477;
Best Local Similarity 28.1%; Pred. No. 1.6e+02;
RESULT 262
ID ABP97372 standard; protein; 1512 AA.
DE Human kielin-like protein NHP5, SEQ ID NO:10.
PN WO2003004609-A2.
PD 16-JAN-2003.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 7.8%; Score 80.5; DB 6; Length 1512;
Best Local Similarity 28.1%; Pred. No. 1.6e+02;
RESULT 263
ID ABP97374 standard; protein; 1535 AA.
DE Human kielin-like protein NHP7, SEQ ID NO:14.
PN WO2003004609-A2.
PD 16-JAN-2003.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 7.8%; Score 80.5; DB 6; Length 1535;
Best Local Similarity 28.1%; Pred. No. 1.7e+02;
RESULT 264
ID ABP97373 standard; protein; 1570 AA.
DE Human kielin-like protein NHP6, SEQ ID NO:12.
PN WO2003004609-A2.
PD 16-JAN-2003.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 7.8%; Score 80.5; DB 6; Length 1570;
Best Local Similarity 28.1%; Pred. No. 1.7e+02;
RESULT 265
ID ABP97369 standard; protein; 1593 AA.
DE Human kielin-like protein NHP2, SEQ ID NO:4.
PN WO2003004609-A2.
PD 16-JAN-2003.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 7.8%; Score 80.5; DB 6; Length 1593;
Best Local Similarity 28.1%; Pred. No. 1.8e+02;
RESULT 266
ID ABP97368 standard; protein; 1628 AA.
DE Human kielin-like protein NHP1, SEQ ID NO:2.
PN WO2003004609-A2.
PD 16-JAN-2003.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 7.8%; Score 80.5; DB 6; Length 1628;
Best Local Similarity 28.1%; Pred. No. 1.8e+02;
RESULT 267
ID ABG06003 standard; protein; 1076 AA.
DE Novel human diagnostic protein #5994.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.7%; Score 80; DB 4; Length 1076;
Best Local Similarity 23.5%; Pred. No. 1.2e+02;
RESULT 268
ID ADN96164 standard; protein; 489 AA.
DE Human NOVX polypeptide #109.
PN US2004067490-A1.
PD 08-APR-2004.
PA (ZHON/) ZHONG M.
PA (LILL/) LI L.
PA (GORM/) GORMAN L.
PA (SPVT/) SPYTEK K A.
PA (KEKU/) KEKUDA R.
PA (TAUP/) TAUPIER R J.
PA (ANDE/) ANDERSON D W.
PA (VERN/) VERNET C A M.
PA (CATT/) CATTERTON E.
PA (MILL/) MILLER C E.
PA (SHEN/) SHENOV S G.
PA (PAIT/) PAITTURAJAN M.
PA (PENA/) PENNA C E A.
PA (TCHER/) TCHERNEV V T.
PA (PADI/) PADIGARU M.
PA (GUSE/) GUSEV V Y.
PA (MALY/) MALYANKAR U M.
PA (BURG/) BURGESS C E.
PA (GERL/) GERLACH V.
PA (CASW/) CASMAN S J.

PA (RIEG//) RIEGER D K.
 PA (GROS//) GROSSE W M.
 PA (SMIT//) SMITHSON G.
 PA (PEYM//) PEYMAN J A.
 PA (STAR//) STARLING G.
 PA (ROTH//) ROTHENBERG M E.
 PA (LARO//) LAROCHELLE W J.
 PA (SHIM//) SHIMKETS R A.
 PA (CRAB//) CRABTREE J.
 PA (RAST//) RASTELLI L.
 PA (VOSS//) VOSS E Z.
 PA (BOLD//) BOLDOG F L.
 PA (EDIN//) EDINGER S R.
 PA (MILL//) MILLET I.
 PA (MACD//) MACDOUGALL J R.
 PA (ELLE//) ELLERMAN K.
 PA (CHAP//) CHAPOVAL A.
 Query Match 7.7%; Score 79.5; DB 8; Length 489;
 Best Local Similarity 23.5%; Pred. No. 44;
 RESULT 269
 ID ANM38983 standard; protein; 497 AA.
 DE Human polypeptide SEQ ID NO 2128.
 PN WO200153312-A1.
 PD 26-JUL-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 7.6%; Score 79; DB 4; Length 497;
 Best Local Similarity 22.8%; Pred. No. 51;
 RESULT 270
 ID ABM82186 standard; protein; 510 AA.
 DE Tumour-associated antigenic target (TAT) polypeptide PRO83107, SEQ:5637.
 PN WO2004030615-A2.
 PD 15-APR-2004.
 PA (GETH//) GENENTECH INC.
 Query Match 7.6%; Score 79; DB 8; Length 510;
 Best Local Similarity 22.8%; Pred. No. 53;
 RESULT 271
 ID ADL06716 standard; protein; 105 AA.
 DE Human brachydactyly-body height IHH exon 1protein.
 PN CN1343773-A.
 PD 10-APR-2002.
 PA (UYSH-) UNIV SHANGHAI JIAOTONG.
 Query Match 7.6%; Score 78.5; DB 7; Length 105;
 Best Local Similarity 26.4%; Pred. No. 6.8;
 RESULT 272
 ID ADP76160 standard; protein; 273 AA.
 DE Tobacco STZ orthologue osmotic stress-induced zfp, SEQ ID NO:17.
 PN WO2004058980-A2.
 PD 15-JUL-2004.
 PA (CROP-) CROPDISEIGN NV.
 Query Match 7.6%; Score 78.5; DB 8; Length 273;
 Best Local Similarity 23.5%; Pred. No. 25;
 RESULT 273
 ID ANM40722 standard; protein; 444 AA.
 DE Human polypeptide SEQ ID NO 5653.
 PN WO200153312-A1.
 PD 26-JUL-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 7.5%; Score 78; DB 4; Length 444;
 Best Local Similarity 28.4%; Pred. No. 56;
 RESULT 274
 ID ABB59659 standard; protein; 448 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 5769.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE//) PE CORP NY.
 Query Match 7.5%; Score 78; DB 4; Length 448;
 Best Local Similarity 39.6%; Pred. No. 56;
 RESULT 275
 ID ADL06714 standard; protein; 105 AA.
 DE Human brachydactyly-body height IHH exon 1derived protein.
 PN CN1343773-A.
 PD 10-APR-2002.
 PA (UYSH-) UNIV SHANGHAI JIAOTONG.

Query Match 7.5%; Score 77.5; DB 7; Length 105;
 Best Local Similarity 29.2%; Pred. No. 8.7;
 RESULT 276
 ID AAG91566 standard; protein; 169 AA.
 DE C glutamicum protein fragment SEQ ID NO: 5320.
 PN EPI108790-A2.
 PD 20-JUN-2001.
 PA (KYOW//) KYOWA HAKKO KOGYO KK.
 Query Match 7.5%; Score 77.5; DB 4; Length 169;
 Best Local Similarity 23.4%; Pred. No. 17;
 RESULT 277
 ID AAM79890 standard; protein; 432 AA.
 DE Human protein SEQ ID NO 3536.
 PN WO200157190-A2.
 PD 09-AUG-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 7.5%; Score 77.5; DB 4; Length 432;
 Best Local Similarity 22.5%; Pred. No. 60;
 RESULT 278
 ID AAM41175 standard; protein; 432 AA.
 DE Human polypeptide SEQ ID NO 6106.
 PN WO200153312-A1.
 PD 26-JUL-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 7.5%; Score 77.5; DB 4; Length 432;
 Best Local Similarity 22.5%; Pred. No. 60;
 RESULT 279
 ID ABM84884 standard; protein; 663 AA.
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:5133.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 7.5%; Score 77.5; DB 8; Length 663;
 Best Local Similarity 22.4%; Pred. No. 1.1e+02;
 RESULT 280
 ID ABB97515 standard; protein; 277 AA.
 DE Novel human protein SEQ ID NO: 783.
 PN WO200222660-A2.
 PD 21-MAR-2002.
 PA (HYSE-) HYSEQ INC.
 Query Match 7.4%; Score 77; DB 5; Length 277;
 Best Local Similarity 20.1%; Pred. No. 37;
 RESULT 281
 ID ADM87387 standard; protein; 545 AA.
 DE Human protein SEQ ID NO:480.
 PN WO2004009834-A2.
 PD 29-JAN-2004.
 PA (NUVE-) NUVELO INC.
 Query Match 7.4%; Score 77; DB 8; Length 545;
 Best Local Similarity 20.1%; Pred. No. 93;
 RESULT 282
 ID ADP30057 standard; protein; 578 AA.
 DE Human secreted protein SEQ ID #824.
 PN WO2004035732-A2.
 PD 29-APR-2004.
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 Query Match 7.4%; Score 77; DB 8; Length 578;
 Best Local Similarity 25.2%; Pred. No. 1e+02;
 RESULT 283
 ID ABB65565 standard; protein; 820 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 23487.
 PN WO200171042-A2.
 PD 27-SEP-2001
 PA (PEKE//) PE CORP NY.
 Query Match 7.4%; Score 77; DB 4; Length 820;
 Best Local Similarity 18.1%; Pred. No. 1.6e+02;
 RESULT 284
 ID ABB63321 standard; protein; 1783 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 16755.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE//) PE CORP NY.
 Query Match 7.4%; Score 77; DB 4; Length 1783;

Best Local Similarity 21.9%; Pred. No. 4.7e+02;
RESULT 285
ID ADN72815 standard; protein; 2208 AA.
DE Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 710.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDISEIGN NV.
Query Match 7.4%; Score 77; DB 8; Length 2208;
Best Local Similarity 22.3%; Pred. No. 6.3e+02;
RESULT 286
ID ADI45121 standard; protein; 375 AA.
DE Rice isoprenoid biosynthesis-associated protein #26.
PN US2004010815-A1.
PD 15-JAN-2004.
PA (LANG/) LANGE B M.
PA (GHAS/) GHASSEMIAN M.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI P.
PA (KREP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICKÉ D.
PA (ZHUT/) ZHU T.
Query Match 7.4%; Score 76.5; DB 8; Length 375;
Best Local Similarity 24.3%; Pred. No. 63;
RESULT 287
ID ADP29445 standard; protein; 382 AA.
DE Human secreted protein SEQ ID #212.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 7.4%; Score 76.5; DB 8; Length 382;
Best Local Similarity 24.8%; Pred. No. 65;
RESULT 288
ID ADP29438 standard; protein; 550 AA.
DE Human secreted protein SEQ ID #205.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 7.4%; Score 76.5; DB 8; Length 550;
Best Local Similarity 24.8%; Pred. No. 1.1e+02;
RESULT 289
ID ADF43222 standard; protein; 1028 AA.
DE Mouse CRIM1 amino acid sequence SEQ ID NO:14.
PN WO2003101284-A2.
PD 11-DEC-2003.
PA (META-) METABOLEX INC.
Query Match 7.4%; Score 76.5; DB 8; Length 1028;
Best Local Similarity 21.0%; Pred. No. 2.5e+02;
RESULT 290
ID AAU07142 standard; protein; 1037 AA.
DE Mouse CRIM1 protein.
PN WO200138519-A1.
PD 31-MAY-2001.
PA (UYQU) UNIV QUEENSLAND.
Query Match 7.4%; Score 76.5; DB 4; Length 1037;
Best Local Similarity 21.0%; Pred. No. 2.5e+02;
RESULT 291
ID ABP62761 standard; protein; 5754 AA.
DE S. roseosporus daptomycin non-ribosomal peptide synthetase DptA.
PN WO200259322-A2.
PD 01-AUG-2002.
PA (MIAO/) MIAO V P W.
PA (BRJA/) BRIAN P. W.
PA (BALT/) BALTZ R H.
PA (SILV/) SILVA C J.
Query Match 7.4%; Score 76.5; DB 5; Length 5754;
Best Local Similarity 29.1%; Pred. No. 2.7e+03;
RESULT 292
ID ADJ72173 standard; protein; 5830 AA.

DE Streptomyces roseosporus DptA protein.
PN WO2003014297-A2.
PD 20-FEB-2003.
PA (CUBI-) CUBIST PHARM INC.
Query Match 7.4%; Score 76.5; DB 7; Length 5830;
Best Local Similarity 29.1%; Pred. No. 2.7e+03;
RESULT 293
ID ABB71438 standard; protein; 202 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 41106.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.3%; Score 76; DB 4; Length 202;
Best Local Similarity 25.9%; Pred. No. 30;
RESULT 294
ID ADK17005 standard; protein; 313 AA.
DE Nanarchaeum equitans cancer-associated (CA) protein #478.
PN WO2003093434-A2.
PD 13-NOV-2003.
PA (DIVE-) DIVERSA CORP.
Query Match 7.3%; Score 76; DB 8; Length 313;
Best Local Similarity 42.4%; Pred. No. 55;
RESULT 295
ID AAB68083 standard; protein; 397 AA.
DE Amino acid sequence of a murine orthologue of chordin-like homologue.
PN WO200134796-A1.
PD 17-MAY-2001.
PA (COMP-) COMPUGEN LTD.
Query Match 7.3%; Score 76; DB 4; Length 397;
Best Local Similarity 82.4%; Pred. No. 77;
RESULT 296
ID ABM84887 standard; protein; 625 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5136.
PN WO2004023373-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.3%; Score 76; DB 8; Length 625;
Best Local Similarity 25.7%; Pred. No. 1.4e+02;
RESULT 297
ID ABG04589 standard; protein; 640 AA.
DE Novel human diagnostic protein #4580.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.3%; Score 76; DB 4; Length 640;
Best Local Similarity 27.1%; Pred. No. 1.5e+02;
RESULT 298
ID AAG67415 standard; protein; 1184 AA.
DE Amino acid sequence of bimc polypeptide.
PN US6284480-B1.
PD 04-SEP-2001.
PA (CYTO-) CYTOKINETICS INC.
Query Match 7.3%; Score 76; DB 4; Length 1184;
Best Local Similarity 23.3%; Pred. No. 3.4e+02;
RESULT 299
ID ABG72690 standard; protein; 1184 AA.
DE A. nidulans BimC, a Kinesin related protein.
PN US6468760-B1.
PD 22-OCT-2002.
PA (CYTO-) CYTOKINETICS INC.
Query Match 7.3%; Score 76; DB 6; Length 1184;
Best Local Similarity 23.3%; Pred. No. 3.4e+02;
RESULT 300
ID ADG98956 standard; protein; 1184 AA.
DE Fungal bimc polypeptide.
PN US6627408-B1.
PD 30-SEP-2003.
PA (CYTO-) CYTOKINETICS INC.
Query Match 7.3%; Score 76; DB 7; Length 1184;
Best Local Similarity 23.3%; Pred. No. 3.4e+02;
RESULT 301
ID ABG21542 standard; protein; 445 AA.
DE Novel human diagnostic protein #21533.

PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.3%; Score 75.5; DB 4; Length 445;
Best Local Similarity 26.9%; Pred. No. 1e+02;
RESULT 302
ID ADG76976 standard; protein; 744 AA.
DE Human nucleic acid associated polypeptide (NAAP) 4.
PN WO2003076586-A2.
PD 18-SEP-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 7.3%; Score 75.5; DB 7; Length 744;
Best Local Similarity 22.1%; Pred. No. 2e+02;
RESULT 303
ID AAG35015 standard; protein; 111 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 42706.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 7.2%; Score 75; DB 3; Length 111;
Best Local Similarity 38.5%; Pred. No. 17;
RESULT 304
ID AAG35014 standard; protein; 114 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 42705.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 7.2%; Score 75; DB 3; Length 114;
Best Local Similarity 38.5%; Pred. No. 18;
RESULT 305
ID ABB04642 standard; protein; 338 AA.
DE Human BOLA structural domain zinc finger protein 37 SEQ ID NO: 2.
PN CN1307053-A.
PD 08-AUG-2001.
PA (BODA-) BODAO GENE TECH CO LTD SHANGHAI.
Query Match 7.2%; Score 75; DB 5; Length 338;
Best Local Similarity 20.2%; Pred. No. 78;
RESULT 306
ID ADP67675 standard; protein; 374 AA.
DE Novel human protein sequence #2341.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 7.2%; Score 75; DB 8; Length 374;
Best Local Similarity 21.8%; Pred. No. 90;
RESULT 307
ID AAB73600 standard; protein; 513 AA.
DE Zinc finger protein 57.
PN WO200130840-A1.
PD 03-MAY-2001.
PA (SHAN-) SHANGHAI BIO ROAD GENE DEV LTD.
Query Match 7.2%; Score 75; DB 4; Length 513;
Best Local Similarity 20.1%; Pred. No. 1.4e+02;
RESULT 308
ID ABB54028 standard; protein; 72 AA.
DE Lactococcus lactis protein yhcC.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG-) INRA INST NAT RECH AGRONOMIQUE.
Query Match 7.2%; Score 74.5; DB 5; Length 72;
Best Local Similarity 30.4%; Pred. No. 11;
RESULT 309
ID ABR41677 standard; protein; 240 AA.
DE Human DITHP cell membrane protein.
PN WO200297031-A2.
PD 05-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 7.2%; Score 74.5; DB 6; Length 240;
Best Local Similarity 23.4%; Pred. No. 55;
RESULT 310
ID ABG07985 standard; protein; 562 AA.
DE Novel human diagnostic protein #7976.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.

Query Match 7.2%; Score 74.5; DB 4; Length 562;
Best Local Similarity 24.2%; Pred. No. 1.8e+02;
RESULT 311
ID AAE05111 standard; protein; 1065 AA.
DE Human diacylglycerol kinase (DGK) iota protein.
PN US6255095-B1.
PD 03-JUL-2001.
PA (UTAH-) UNIV UTAH RES FOUND.
Query Match 7.2%; Score 74.5; DB 4; Length 1065;
Best Local Similarity 23.0%; Pred. No. 4.2e+02;
RESULT 312
ID ADJ68776 standard; protein; 1065 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID582.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 7.2%; Score 74.5; DB 7; Length 1065;
Best Local Similarity 23.0%; Pred. No. 4.2e+02;
RESULT 313
ID ADQ19889 standard; protein; 1065 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2708.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 7.2%; Score 74.5; DB 8; Length 1065;
Best Local Similarity 23.0%; Pred. No. 4.2e+02;
RESULT 314
ID ADR19331 standard; protein; 219 AA.
DE Chimeric mouse/human antibody IgG1 or IgM kappa light chain, c1gG-Pankol.
PN WO2004065423-A2.
PD 05-AUG-2004.
PA (NEMO-) NEMOD BIOTHERAPEUTICS GMBH & CO KG.
Query Match 7.1%; Score 74; DB 8; Length 219;
Best Local Similarity 24.4%; Pred. No. 55;
RESULT 315
ID AAB73602 standard; protein; 220 AA.
DE Human zinc finger protein ZNFPT1 fragment (residues 67-286).
PN WO200130840-A1.
PD 03-MAY-2001.
PA (SHAN-) SHANGHAI BIO ROAD GENE DEV LTD.
Query Match 7.1%; Score 74; DB 4; Length 220;
Best Local Similarity 20.1%; Pred. No. 55;
RESULT 316
ID ADQ20492 standard; protein; 227 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 3312.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 7.1%; Score 74; DB 8; Length 227;
Best Local Similarity 20.1%; Pred. No. 58;
RESULT 317
ID ADS88785 standard; protein; 238 AA.
DE Sequence of the chimeric IC2 kappa light chain in M13mp19 clone M609.
PN WO2004083373-A2.
PD 30-SEP-2004.
PA (UYNE-) UNIV NEWCASTLE-UPON-TYNE.
Query Match 7.1%; Score 74; DB 8; Length 238;
Best Local Similarity 24.4%; Pred. No. 61;
RESULT 318
ID ADS43814 standard; protein; 239 AA.
DE Bacterial polypeptide #22244.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY-) CAO Y.
PA (HINK-) HINKLE G J.
PA (SLAT-) SLATER S C.
PA (CHEN-) CHEN X.
PA (GOLD-) GOLDMAN B S.
Query Match 7.1%; Score 74; DB 8; Length 239;
Best Local Similarity 25.8%; Pred. No. 62;
RESULT 319
ID ADG63079 standard; protein; 524 AA.

DE Mouse glycerol kinase GLK #2.
 PN US2003208057-A1.
 PD 06-NOV-2003.
 PA (LEWI/) LEWIN D A.
 PA (STEW/) STEWART T A.
 Query Match 7.1%; Score 74; DB 7; Length 524;
 Best Local Similarity 21.7%; Pred. No. 1.8e+02;
 RESULT 320
 ID ADJ76376 standard; protein; 524 AA.
 DE Marker gene related amino acid sequence SEQ ID NO:1628.
 PN EP1394274-A2.
 PD 03-MAR-2004.
 PA (GENO-) GENOX RES INC.
 Query Match 7.1%; Score 74; DB 8; Length 524;
 Best Local Similarity 21.7%; Pred. No. 1.8e+02;
 RESULT 321
 ID ABJ37102 standard; protein; 608 AA.
 DE Concatameric immunoadhesion human protein sequence SEQ ID No 10.
 PN WO2003010202-A1.
 PD 06-FEB-2003.
 PA (MEDE-) MEDEXGEN CO LTD.
 Query Match 7.1%; Score 74; DB 6; Length 608;
 Best Local Similarity 23.4%; Pred. No. 2.2e+02;
 RESULT 322
 ID AD079908 standard; protein; 608 AA.
 DE Human tumour necrosis factor receptor 1, mgTNFRI-TNFR1/Ig construct.
 PN KR2004009997-A.
 PD 31-JAN-2004.
 PA (MEDE-) MEDEXGEN INC.
 Query Match 7.1%; Score 74; DB 8; Length 608;
 Best Local Similarity 23.4%; Pred. No. 2.2e+02;
 RESULT 323
 ID ABB54564 standard; protein; 710 AA.
 DE Lactococcus lactis protein topa.
 PN FR280746-A1.
 PD 12-OCT-2001.
 PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
 Query Match 7.1%; Score 74; DB 5; Length 710;
 Best Local Similarity 29.0%; Pred. No. 2.7e+02;
 RESULT 324
 ID ADS29382 standard; protein; 710 AA.
 DE Bacterial polypeptide #18415.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Query Match 7.1%; Score 74; DB 8; Length 710;
 Best Local Similarity 29.0%; Pred. No. 2.7e+02;
 RESULT 325
 ID AAR22461 standard; protein; 1712 AA.
 DE Masking protein high polymer unit precursor MPU-P.
 PN JP04066597-A.
 PD 02-MAR-1992.
 PA (NAGA/) NAKAMURA T.
 Query Match 7.1%; Score 74; DB 2; Length 1712;
 Best Local Similarity 20.4%; Pred. No. 9.2e+02;
 RESULT 326
 ID ADE61336 standard; protein; 1712 AA.
 DE Rat Protein Q00918, SEQ ID NO 7254.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 7.1%; Score 74; DB 7; Length 1712;
 Best Local Similarity 20.4%; Pred. No. 9.2e+02;
 RESULT 327
 ID AAW54235 standard; peptide; 3224 AA.
 DE Human Nup358 protein.
 PN WO9809170-A2.
 PD 05-MAR-1998.

PA (MATR-) MATRITECH INC.
 Query Match 7.1%; Score 74; DB 2; Length 3224;
 Best Local Similarity 20.8%; Pred. No. 2.2e+03;
 RESULT 328
 ID ABO14790 standard; protein; 3224 AA.
 DE Novel human protein #163.
 PN WO2003023002-A2.
 PD 20-MAR-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 7.1%; Score 74; DB 6; Length 3224;
 Best Local Similarity 20.8%; Pred. No. 2.2e+03;
 RESULT 329
 ID ADO23719 standard; protein; 3224 AA.
 DE Nup358, SEQ ID 8.
 PN WO2004027381-A2.
 PD 01-APR-2004.
 PA (UTAH) UNIV UTAH RES FOUND.
 Query Match 7.1%; Score 74; DB 8; Length 3224;
 Best Local Similarity 20.8%; Pred. No. 2.2e+03;
 RESULT 330
 ID AAG17855 standard; protein; 158 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 19034.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 7.1%; Score 73.5; DB 3; Length 158;
 Best Local Similarity 26.0%; Pred. No. 40;
 RESULT 331
 ID ADR08117 standard; protein; 165 AA.
 DE Novel protein (useful for identifying genetic disorders) #272.
 PN WO2003054152-A2.
 PD 03-JUL-2003.
 PA (HYSE-) HYSEQ INC.
 Query Match 7.1%; Score 73.5; DB 7; Length 165;
 Best Local Similarity 23.8%; Pred. No. 42;
 RESULT 332
 ID ABU11644 standard; protein; 172 AA.
 DE Human MDDT polypeptide SEQ ID 591.
 PN WO200279449-A2.
 PD 10-OCT-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 7.1%; Score 73.5; DB 6; Length 172;
 Best Local Similarity 31.0%; Pred. No. 44;
 RESULT 333
 ID AAG17854 standard; protein; 176 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 19033.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 7.1%; Score 73.5; DB 3; Length 176;
 Best Local Similarity 26.0%; Pred. No. 46;
 RESULT 334
 ID AAG17853 standard; protein; 198 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 19032.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 7.1%; Score 73.5; DB 3; Length 198;
 Best Local Similarity 26.0%; Pred. No. 54;
 RESULT 335
 ID AAY58149 standard; protein; 223 AA.
 DE Penicillium funiculosum xyranase C.
 PN WO9957325-A2.
 PD 11-NOV-1999.
 PA (RHON) RHONE-POULENC ANIMAL NUTRITION SA.
 PA (RHOD) RHODIA CHIM.
 Query Match 7.1%; Score 73.5; DB 3; Length 223;
 Best Local Similarity 20.9%; Pred. No. 63;
 RESULT 336
 ID ABB79117 standard; protein; 373 AA.
 DE Mutant subtilisin BPN' protein S88 Li261.
 PN WO200226956-A1.
 PD 04-APR-2002.
 PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
 Query Match 7.1%; Score 73.5; DB 5; Length 373;
 Best Local Similarity 21.1%; Pred. No. 1.3e+02;

RESULT 337
ID ABB79098 standard; protein; 373 AA.
DE Mutant subtilisin BPN' protein S88 S189P.
FN WO200226956-A1.
PD 04-APR-2002.
PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
Query Match 7.1%; Score 73.5; DB 5; Length 373;
Best Local Similarity 21.1%; Pred. No. 1.3e+02;
RESULT 338
ID ABB79097 standard; protein; 373 AA.
DE Mutant subtilisin BPN' protein S88.
FN WO200226956-A1.
PD 04-APR-2002.
PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
Query Match 7.1%; Score 73.5; DB 5; Length 373;
Best Local Similarity 21.1%; Pred. No. 1.3e+02;
RESULT 339
ID ABB79120 standard; protein; 373 AA.
DE Mutant subtilisin BPN' protein S88 G169A.
FN WO200226956-A1.
PD 04-APR-2002.
PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
Query Match 7.1%; Score 73.5; DB 5; Length 373;
Best Local Similarity 21.1%; Pred. No. 1.3e+02;
RESULT 340
ID ABB79115 standard; protein; 373 AA.
DE Mutant subtilisin BPN' protein S88 S9A.
FN WO200226956-A1.
PD 04-APR-2002.
PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
Query Match 7.1%; Score 73.5; DB 5; Length 373;
Best Local Similarity 21.1%; Pred. No. 1.3e+02;
RESULT 341
ID ABB79121 standard; protein; 373 AA.
DE Mutant subtilisin BPN' protein S88 N212G.
FN WO200226956-A1.
PD 04-APR-2002.
PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
Query Match 7.1%; Score 73.5; DB 5; Length 373;
Best Local Similarity 21.1%; Pred. No. 1.3e+02;
RESULT 342
ID ABB79122 standard; protein; 373 AA.
DE Mutant subtilisin BPN' protein S88 M222Q.
FN WO200226956-A1.
PD 04-APR-2002.
PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
Query Match 7.1%; Score 73.5; DB 5; Length 373;
Best Local Similarity 21.1%; Pred. No. 1.3e+02;
RESULT 343
ID ABB79125 standard; protein; 373 AA.
DE Mutant subtilisin BPN' protein S88 combined mutations.
FN WO200226956-A1.
PD 04-APR-2002.
PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
Query Match 7.1%; Score 73.5; DB 5; Length 373;
Best Local Similarity 21.1%; Pred. No. 1.3e+02;
RESULT 344
ID ABB79119 standard; protein; 373 AA.
DE Mutant subtilisin BPN' protein S88 G166S.
FN WO200226956-A1.
PD 04-APR-2002.
PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
Query Match 7.1%; Score 73.5; DB 5; Length 373;
Best Local Similarity 21.1%; Pred. No. 1.3e+02;
RESULT 345
ID ABB79124 standard; protein; 373 AA.
DE Mutant subtilisin BPN' protein S88 T254A.
FN WO200226956-A1.
PD 04-APR-2002.
PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
Query Match 7.1%; Score 73.5; DB 5; Length 373;
Best Local Similarity 21.1%; Pred. No. 1.3e+02;
RESULT 346
ID ABB79123 standard; protein; 373 AA.
DE Mutant subtilisin BPN' protein S88 S189P.
FN WO200226956-A1.
PD 04-APR-2002.
PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
Query Match 7.1%; Score 73.5; DB 5; Length 373;
Best Local Similarity 21.1%; Pred. No. 1.3e+02;
RESULT 347
ID ABB79116 standard; protein; 373 AA.
DE Mutant subtilisin BPN' protein S88 I31L.
FN WO200226956-A1.
PD 04-APR-2002.
PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
Query Match 7.1%; Score 73.5; DB 5; Length 373;
Best Local Similarity 21.1%; Pred. No. 1.3e+02;
RESULT 348
ID ABB79118 standard; protein; 373 AA.
DE Mutant subtilisin BPN' protein S88 E156S.
FN WO200226956-A1.
PD 04-APR-2002.
PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
Query Match 7.1%; Score 73.5; DB 5; Length 373;
Best Local Similarity 21.1%; Pred. No. 1.3e+02;
RESULT 349
ID AAB95766 standard; protein; 611 AA.
DE Human protein sequence SEQ ID NO:18697.
FN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 7.1%; Score 73.5; DB 4; Length 611;
Best Local Similarity 24.2%; Pred. No. 2.5e+02;
RESULT 350
ID ADJ80164 standard; protein; 643 AA.
DE Novel human nucleic acid-associated protein #40.
FN WO2003038052-A2.
PD 08-MAY-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 7.1%; Score 73.5; DB 7; Length 643;
Best Local Similarity 24.2%; Pred. No. 2.7e+02;
RESULT 351
ID ABG21359 standard; protein; 1233 AA.
DE Novel human diagnostic protein #21350.
FN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.1%; Score 73.5; DB 4; Length 1233;
Best Local Similarity 21.6%; Pred. No. 6.6e+02;
RESULT 352
ID AAU00874 standard; protein; 142 AA.
DE Human cancer related protein 9.
FN WO200118014-A1.
PD 15-MAR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.0%; Score 73; DB 4; Length 142;
Best Local Similarity 51.4%; Pred. No. 38;
RESULT 353
ID ADQ82997 standard; protein; 193 AA.
DE Human CRP1, SEQ ID 3.
FN WO2004062474-A2.
PD 29-JUL-2004.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
Query Match 7.0%; Score 73; DB 8; Length 193;
Best Local Similarity 20.5%; Pred. No. 59;
RESULT 354
ID ARAG42698 standard; protein; 230 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 53279.
FN EPI033405-A2.
PD 06-SEP-2000.
Query Match 7.0%; Score 73; DB 3; Length 230;
Best Local Similarity 24.4%; Pred. No. 75;
RESULT 355
ID ABB91706 standard; protein; 230 AA.
DE Herbicidally active polypeptide SEQ ID NO 917.

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PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB ) BAYER AG.
Query Match 7.0%; Score 73; DB 5; Length 230;
Best Local Similarity 24.4%; Pred. No. 75;
RESULT 356
ID AAB44500 standard; protein; 258 AA.
DE Plant viral movement protein SEQ ID 14.
PN WO200060088-A2.
PD 12-OCT-2000.
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
Query Match 7.0%; Score 73; DB 3; Length 258;
Best Local Similarity 27.6%; Pred. No. 87;
RESULT 357
ID ABG08174 standard; protein; 396 AA.
DE Novel human diagnostic protein #8165.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.0%; Score 73; DB 4; Length 396;
Best Local Similarity 21.8%; Pred. No. 1.6e+02;
RESULT 358
ID ABG08179 standard; protein; 403 AA.
DE Novel human diagnostic protein #8170.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.0%; Score 73; DB 4; Length 403;
Best Local Similarity 21.8%; Pred. No. 1.6e+02;
RESULT 359
ID AAB5092 standard; protein; 449 AA.
DE Mouse indian hedgehog (ihh) polypeptide.
PN WO200141786-A1.
PD 14-JUN-2001.
PA (GEO ) GEN HOSPITAL CORP.
Query Match 7.0%; Score 73; DB 4; Length 449;
Best Local Similarity 26.2%; Pred. No. 1.9e+02;
RESULT 360
ID AAE19838 standard; protein; 449 AA.
DE Mouse indian hedgehog (ihh) protein.
PN US6348575-B1.
PD 19-FEB-2002.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 73; DB 5; Length 449;
Best Local Similarity 26.2%; Pred. No. 1.9e+02;
RESULT 361
ID ABG74112 standard; protein; 449 AA.
DE Mouse indian hedgehog protein.
PN US2002156245-A1.
PD 24-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 73; DB 6; Length 449;
Best Local Similarity 26.2%; Pred. No. 1.9e+02;
RESULT 362
ID ABB67836 standard; protein; 457 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 30300.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 7.0%; Score 73; DB 4; Length 457;
Best Local Similarity 21.7%; Pred. No. 1.9e+02;
RESULT 363
ID ABR53280 standard; protein; 1244 AA.
DE Protein sequence #SEQ ID 1425.
PN EP1258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match 7.0%; Score 73; DB 6; Length 1244;
Best Local Similarity 23.0%; Pred. No. 7.5e+02;
RESULT 364
ID ADK63590 standard; protein; 1244 AA.
DE Disease treating protein complex-derived protein #858.
PN EP1338608-A2.

PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 7.0%; Score 73; DB 7; Length 1244;
Best Local Similarity 23.0%; Pred. No. 7.5e+02;
RESULT 365
ID ADN18772 standard; protein; 1244 AA.
DE Bacterial polypeptide #1425.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 7.0%; Score 73; DB 8; Length 1244;
Best Local Similarity 23.0%; Pred. No. 7.5e+02;
RESULT 366
ID ABG79171 standard; protein; 1427 AA.
DE Human von willebrand factor and kielin-like protein.
PN WO200264791-A2.
PD 22-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.0%; Score 73; DB 5; Length 1427;
Best Local Similarity 31.4%; Pred. No. 9.1e+02;
RESULT 367
ID ABU31130 standard; protein; 2399 AA.
DE Protein encoded by Prokaryotic essential gene #16657.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.0%; Score 73; DB 6; Length 2399;
Best Local Similarity 23.1%; Pred. No. 1.8e+03;
RESULT 368
ID ABU26086 standard; protein; 144 AA.
DE Protein encoded by Prokaryotic essential gene #11613.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.0%; Score 72.5; DB 6; Length 144;
Best Local Similarity 35.2%; Pred. No. 44;
RESULT 369
ID ABU96699 standard; protein; 494 AA.
DE Human nucleic acid-associated protein (NAAP) #28.
PN WO2003023003-A2.
PD 20-MAR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 7.0%; Score 72.5; DB 6; Length 494;
Best Local Similarity 21.2%; Pred. No. 2.4e+02;
RESULT 370
ID ABB71195 standard; protein; 602 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 40377.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 7.0%; Score 72.5; DB 4; Length 602;
Best Local Similarity 20.9%; Pred. No. 3.1e+02;
RESULT 371
ID ADN99703 standard; protein; 673 AA.
DE Novel human protein sequence #519.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 7.0%; Score 72.5; DB 8; Length 673;
Best Local Similarity 25.5%; Pred. No. 3.7e+02;
RESULT 372
ID AAB94388 standard; protein; 675 AA.
DE Human protein sequence SEQ ID NO:14947.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 7.0%; Score 72.5; DB 4; Length 675;
Best Local Similarity 25.5%; Pred. No. 3.7e+02;
RESULT 373
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ID ABG17368 standard; protein; 714 AA.
DE Novel human diagnostic protein #17359.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.0%; Score 72.5; DB 4; Length 714;
Best Local Similarity 25.5%; Pred. No. 4e+02;
RESULT 374
ID ANM79223 standard; protein; 766 AA.
DE Human protein SEQ ID NO 1885.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 7.0%; Score 72.5; DB 4; Length 766;
RESULT 375
ID ABG07025 standard; protein; 795 AA.
DE Novel human diagnostic protein #7016.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 7.0%; Score 72.5; DB 4; Length 795;
RESULT 376
ID ABU96693 standard; protein; 798 AA.
DE Human nucleic acid-associated protein (NAAP) #22.
PN WO2003032003-A2.
PD 20-MAR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 7.0%; Score 72.5; DB 6; Length 798;
Best Local Similarity 22.0%; Pred. No. 4.6e+02;
RESULT 377
ID AAM80207 standard; protein; 852 AA.
DE Human protein SEQ ID NO 3853.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.0%; Score 72.5; DB 4; Length 852;
Best Local Similarity 22.0%; Pred. No. 5e+02;
RESULT 378
ID ABG28743 standard; protein; 1196 AA.
DE Novel human diagnostic protein #28734.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.0%; Score 72.5; DB 4; Length 1196;
Best Local Similarity 22.8%; Pred. No. 8e+02;
RESULT 379
ID ABG32652 standard; protein; 1476 AA.
DE P. luminescens (W-14) TcdB protein.
PN US2002078478-A1.
PD 20-JUN-2002.
PA (FFRE/) FFRENCH-CONSTANT R. H.
PA (BOWE/) BOWEN D.
PA (ROCH/) ROCHELEAU T. A.
PA (WATE/) WATERFIELD N. R.
Query Match 7.0%; Score 72.5; DB 5; Length 1476;
Best Local Similarity 25.0%; Pred. No. 1.1e+03;
RESULT 380
ID ADK21576 standard; protein; 1476 AA.
DE Photorhabdus TcdB1 toxin.
PN WO2004067727-A2.
PD 12-AUG-2004.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 7.0%; Score 72.5; DB 8; Length 1476;
Best Local Similarity 25.0%; Pred. No. 1.1e+03;
RESULT 381
ID ABP33206 standard; protein; 138 AA.
DE Human ORF2179 protein, SEQ ID NO:4358.
PN WO200190366-A2.
PD 29-NOV-2001.
PA (CURA-) CURAGEN CORP.
Query Match 6.9%; Score 72; DB 5; Length 138;

Best Local Similarity 26.7%; Pred. No. 47;
RESULT 382
ID ABB59215 standard; protein; 197 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 4437.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.9%; Score 72; DB 4; Length 197;
Best Local Similarity 23.5%; Pred. No. 77;
RESULT 383
ID ADP84971 standard; protein; 219 AA.
DE Chimeric antibody cIGG-Karo4.
PN WO2004050707-A2.
PD 17-JUN-2004.
PA (NEMO-) NEMOD BIOTHERAPEUTICS GMBH & CO KG.
Query Match 6.9%; Score 72; DB 8; Length 219;
Best Local Similarity 23.8%; Pred. No. 88;
RESULT 384
ID AAG08690 standard; protein; 230 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 6328.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.9%; Score 72; DB 3; Length 230;
Best Local Similarity 24.4%; Pred. No. 95;
RESULT 385
ID AUB80221 standard; protein; 247 AA.
DE Mycobacterium tuberculosis nutrient starvation-inducible protein #130.
PN WO2003004520-A2.
PD 16-JAN-2003.
PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.
Query Match 6.9%; Score 72; DB 7; Length 247;
Best Local Similarity 24.8%; Pred. No. 1e+02;
RESULT 386
ID AAG13499 standard; protein; 253 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 13016.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.9%; Score 72; DB 3; Length 253;
Best Local Similarity 29.1%; Pred. No. 1.1e+02;
RESULT 387
ID AAG13498 standard; protein; 257 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 13015.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.9%; Score 72; DB 3; Length 257;
Best Local Similarity 29.1%; Pred. No. 1.1e+02;
RESULT 388
ID AAG13497 standard; protein; 264 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 13014.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.9%; Score 72; DB 3; Length 264;
Best Local Similarity 29.1%; Pred. No. 1.1e+02;
RESULT 389
ID AAG08696 standard; protein; 294 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 6336.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.9%; Score 72; DB 3; Length 294;
Best Local Similarity 20.1%; Pred. No. 1.3e+02;
RESULT 390
ID AAG08695 standard; protein; 295 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 6335.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.9%; Score 72; DB 3; Length 295;
Best Local Similarity 20.1%; Pred. No. 1.3e+02;
RESULT 391
ID AAG41543 standard; protein; 333 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 51699.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.9%; Score 72; DB 3; Length 333;

Best Local Similarity 20.3%; Pred. No. 1.6e+02;
RESULT 392
ID ADO61637 standard; protein; 333 AA.
DE Transcription factor G478, SEQ ID 104.
PN WO2004031349-A2.
PD 15-APR-2004.
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
Query Match 6.9%; Score 72; DB 8; Length 333;
Best Local Similarity 20.3%; Pred. No. 1.6e+02;
RESULT 393
ID ABG15502 standard; protein; 342 AA.
DE Novel human diagnostic protein #15493.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.9%; Score 72; DB 4; Length 342;
Best Local Similarity 23.7%; Pred. No. 1.6e+02;
RESULT 394
ID ADS28080 standard; protein; 400 AA.
DE Bacterial polypeptide #17113.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.9%; Score 72; DB 8; Length 400;
Best Local Similarity 21.0%; Pred. No. 2e+02;
RESULT 395
ID AAW94470 standard; protein; 411 AA.
DE Mouse ihh hedgehog protein sequence.
PN WO9900117-A2.
PD 07-JAN-1999.
PA (ONTO-) ONTOGENY INC.
Query Match 6.9%; Score 72; DB 2; Length 411;
Best Local Similarity 26.2%; Pred. No. 2.1e+02;
RESULT 396
ID AAY05856 standard; protein; 411 AA.
DE Mouse Indian hedgehog Ihh protein.
PN WO9920298-A1.
PD 29-APR-1999.
PA (ONTO-) ONTOGENY INC.
Query Match 6.9%; Score 72; DB 2; Length 411;
Best Local Similarity 26.2%; Pred. No. 2.1e+02;
RESULT 397
ID AAW97767 standard; protein; 411 AA.
DE Mouse Indian hedgehog (ihh) protein.
PN WO9904775-A2.
PD 04-FEB-1999.
PA (ONTO-) ONTOGENY INC.
Query Match 6.9%; Score 72; DB 2; Length 411;
Best Local Similarity 26.2%; Pred. No. 2.1e+02;
RESULT 398
ID AAY05512 standard; protein; 411 AA.
DE Mouse Indian hedgehog protein Ihh.
PN WO9910004-A2.
PD 04-MAR-1999.
PA (ONTO-) ONTOGENY INC.
Query Match 6.9%; Score 72; DB 2; Length 411;
Best Local Similarity 26.2%; Pred. No. 2.1e+02;
RESULT 399
ID AAY96245 standard; protein; 411 AA.
DE Mouse Ihh.
PN WO200027422-A2.
PD 18-MAY-2000.
PA (BIOJ-) BIOGEN INC.
PA (ONTO-) ONTOGENY INC.
Query Match 6.9%; Score 72; DB 3; Length 411;
Best Local Similarity 26.2%; Pred. No. 2.1e+02;
RESULT 400
ID AAY70678 standard; protein; 411 AA.
DE Mouse Indian hedgehog (Ihh) protein.

PN WO200015246-A2.
PD 23-MAR-2000.
PA (HARD) HARVARD COLLEGE.
Query Match 6.9%; Score 72; DB 3; Length 411;
Best Local Similarity 26.2%; Pred. No. 2.1e+02;
RESULT 401
ID AAY95283 standard; protein; 411 AA.
DE Mouse Indian hedgehog Ihh protein.
PN WO200035948-A1.
PD 22-JUN-2000.
PA (BIOJ-) BIOGEN INC.
PA (ONTO-) ONTOGENY INC.
Query Match 6.9%; Score 72; DB 3; Length 411;
Best Local Similarity 26.2%; Pred. No. 2.1e+02;
RESULT 402
ID AAY95974 standard; protein; 411 AA.
DE Mouse Indian hedgehog Ihh protein.
PN WO200051628-A2.
PD 08-SEP-2000.
PA (BIOJ-) BIOGEN INC.
Query Match 6.9%; Score 72; DB 3; Length 411;
Best Local Similarity 26.2%; Pred. No. 2.1e+02;
RESULT 403
ID AAB84671 standard; protein; 411 AA.
DE Amino acid sequence of a mouse hedgehog (Ihh) polypeptide.
PN WO200140438-A2.
PD 07-JUN-2001.
PA (CURI-) CURIS INC.
Query Match 6.9%; Score 72; DB 4; Length 411;
Best Local Similarity 26.2%; Pred. No. 2.1e+02;
RESULT 404
ID AAB60262 standard; protein; 411 AA.
DE Mouse Indian hedgehog (Ihh) protein, SEQ ID NO:12.
PN WO200073337-A1.
PD 07-DEC-2000.
PA (BIOJ-) BIOGEN INC.
Query Match 6.9%; Score 72; DB 4; Length 411;
Best Local Similarity 26.2%; Pred. No. 2.1e+02;
RESULT 405
ID AAR04684 standard; protein; 411 AA.
DE Mouse Indian hedgehog (Ihh) protein.
PN WO200134654-A1.
PD 17-MAY-2001.
PA (BIOJ-) BIOGEN INC.
Query Match 6.9%; Score 72; DB 4; Length 411;
Best Local Similarity 26.2%; Pred. No. 2.1e+02;
RESULT 406
ID AAB85735 standard; protein; 411 AA.
DE Mouse Indian hedgehog (Ihh) polypeptide.
PN US6271363-B1.
PD 07-AUG-2001.
PA (HARD) HARVARD COLLEGE.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 6.9%; Score 72; DB 4; Length 411;
Best Local Similarity 26.2%; Pred. No. 2.1e+02;
RESULT 407
ID AAG65745 standard; protein; 411 AA.
DE Mouse Indian hedgehog (Ihh) polypeptide.
PN WO200164238-A2.
PD 07-SEP-2001.
PA (CURI-) CURIS INC.
Query Match 6.9%; Score 72; DB 4; Length 411;
Best Local Similarity 26.2%; Pred. No. 2.1e+02;
RESULT 408
ID AAB31219 standard; protein; 411 AA.
DE Amino acid sequence of mouse Indian hedgehog protein (Ihh).
PN US6165747-A.
PD 26-DEC-2000.
PA (HARD) HARVARD COLLEGE.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 6.9%; Score 72; DB 4; Length 411;
Best Local Similarity 26.2%; Pred. No. 2.1e+02;
RESULT 409

ID ABB79134 standard; protein; 411 AA.
DE Mouse Indian hedgehog (ihh) protein SEQ ID NO:10.
PN USG384192-B1.
PD 07-MAY-2002.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
PA (HARD) HARVARD COLLEGE.
Query Match 6.9%; Score 72; DB 5; Length 411;
Best Local Similarity 26.2%; Pred. No. 2.1e+02;
RESULT 410
ID AAE14294 standard; protein; 411 AA.
DE Mouse Indian hedgehog (ihh) protein.
PN WO200182946-A2.
PD 08-NOV-2001.
PA (CUR1-) CURIS INC.
Query Match 6.9%; Score 72; DB 5; Length 411;
Best Local Similarity 26.2%; Pred. No. 2.1e+02;
RESULT 411
ID AAO20920 standard; protein; 411 AA.
DE Mouse ihh protein sequence SEQ ID No 12.
PN WO200198344-A2.
PD 27-DEC-2001.
PA (BIOJ) BIOGEN INC.
Query Match 6.9%; Score 72; DB 5; Length 411;
Best Local Similarity 26.2%; Pred. No. 2.1e+02;
RESULT 412
ID AAU99480 standard; protein; 411 AA.
DE Mouse Indian hedgehog (ihh) protein.
PN WO200244344-A2.
PD 06-JUN-2002.
PA (CUR1-) CURIS INC.
Query Match 6.9%; Score 72; DB 5; Length 411;
Best Local Similarity 26.2%; Pred. No. 2.1e+02;
RESULT 413
ID ADA26253 standard; protein; 411 AA.
DE Mouse Indian hedgehog (ihh) polypeptide.
PN US2003054437-A1.
PD 20-MAR-2003.
PA (INGH/) INGHAM P W.
PA (MCNA/) MCMAHON A P.
PA (TABI/) TABIN C J.
Query Match 6.9%; Score 72; DB 6; Length 411;
Best Local Similarity 26.2%; Pred. No. 2.1e+02;
RESULT 414
ID ADD25257 standard; protein; 411 AA.
DE Mouse Indian hedgehog (SHH) polypeptide.
PN US6576237-B1.
PD 10-JUN-2003.
PA (HARD) HARVARD COLLEGE.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 6.9%; Score 72; DB 7; Length 411;
Best Local Similarity 26.2%; Pred. No. 2.1e+02;
RESULT 415
ID ABW00865 standard; protein; 411 AA.
DE Mouse Indian hedgehog protein.
PN US2003186357-A1.
PD 02-OCT-2003.
PA (INGH/) INGHAM P W.
PA (MCNA/) MCMAHON A P.
PA (TABI/) TABIN C J.
Query Match 6.9%; Score 72; DB 7; Length 411;
Best Local Similarity 26.2%; Pred. No. 2.1e+02;
RESULT 416
ID ADD71380 standard; protein; 411 AA.
DE Mouse Indian hedgehog (ihh).
PN US2003190696-A1.
PD 09-OCT-2003.
PA (HARD) HARVARD COLLEGE.
Query Match 6.9%; Score 72; DB 7; Length 411;
Best Local Similarity 26.2%; Pred. No. 2.1e+02;
RESULT 417
ID ABW01670 standard; protein; 411 AA.
DE Mouse Indian hedge hog protein.
PN US6630148-B1.

PD 07-OCT-2003.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
PA (HARD) HARVARD COLLEGE.
Query Match 6.9%; Score 72; DB 7; Length 411;
Best Local Similarity 26.2%; Pred. No. 2.1e+02;
RESULT 418
ID ADH61091 standard; protein; 411 AA.
DE Mouse indian hedgehog protein.
PN US6610656-B1.
PD 26-AUG-2003.
PA (HARD) HARVARD COLLEGE.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 6.9%; Score 72; DB 7; Length 411;
Best Local Similarity 26.2%; Pred. No. 2.1e+02;
RESULT 419
ID ADH54654 standard; protein; 411 AA.
DE Mouse Indian hedgehog (Ihh) protein.
PN US6607913-B1.
PD 19-AUG-2003.
PA (INGH/) INGHAM P W.
PA (MCMA/) MCMAHON A P.
PA (TABI/) TABIN C J.
Query Match 6.9%; Score 72; DB 7; Length 411;
Best Local Similarity 26.2%; Pred. No. 2.1e+02;
RESULT 420
ID ADK66378 standard; protein; 411 AA.
DE Mouse indian hedgehog protein.
PN US2003119729-A1.
PD 26-JUN-2003.
PA (MIAO/) MIAO N.
PA (WANG/) WANG M.
PA (MAHA/) MAHANTHAPPA N K.
PA (JINP/) JIN P.
PA (PANG/) PANG K.
Query Match 6.9%; Score 72; DB 7; Length 411;
Best Local Similarity 26.2%; Pred. No. 2.1e+02;
RESULT 421
ID ADH56640 standard; protein; 411 AA.
DE Mouse Indian hedgehog protein sequence SeqID 12.
PN US2003220244-A1.
PD 27-NOV-2003.
PA (WARZ/) WARZECHA J.
Query Match 6.9%; Score 72; DB 8; Length 411;
Best Local Similarity 26.2%; Pred. No. 2.1e+02;
RESULT 422
ID ADK82139 standard; protein; 411 AA.
DE Murine India hedgehog (Ihh) protein.
PN WO2004020599-A2.
PD 11-MAR-2004.
PA (CUR1-) CURIS INC.
Query Match 6.9%; Score 72; DB 8; Length 411;
Best Local Similarity 26.2%; Pred. No. 2.1e+02;
RESULT 423
ID ADR03319 standard; protein; 411 AA.
DE Mouse Indian hedgehog (Ihh) protein.
PN US676788-B1.
PD 27-JUL-2004.
PA (CUR1-) CURIS INC.
Query Match 6.9%; Score 72; DB 8; Length 411;
Best Local Similarity 26.2%; Pred. No. 2.1e+02;
RESULT 424
ID ABO58806 standard; protein; 412 AA.
DE Human genome derived single exon protein #5040.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 6.9%; Score 72; DB 8; Length 412;
Best Local Similarity 24.2%; Pred. No. 2.1e+02;
RESULT 425
ID AAM47938 standard; protein; 441 AA.
DE Human zinc finger protein 49.

PN CNI311210-A.
PD 05-SEP-2001.
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
Query Match Similarity 6.9%; Score 72; DB 5; Length 441;
Best Local Similarity 22.7%; Pred. No. 2.3e+02;
RESULT 426
ID AAE33785 standard; protein; 441 AA.
DE Human nucleic acid associated protein (NAAP)-25.
PN WO200299115-A2.
PD 12-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
PA (YUEH/) YUE H.
Query Match Similarity 6.9%; Score 72; DB 6; Length 441;
Best Local Similarity 23.3%; Pred. No. 2.3e+02;
RESULT 427
ID ADA55416 standard; protein; 441 AA.
DE Human protein, SEQ ID 2984.
PN EPI293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (RRAS-) RES ASSOC BIOTECHNOLOGY.
Query Match Similarity 23.3%; Score 72; DB 6; Length 441;
Best Local Similarity 23.3%; Pred. No. 2.3e+02;
RESULT 428
ID AAU30887 standard; protein; 443 AA.
DE Novel human secreted protein #1378.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match Similarity 6.9%; Score 72; DB 4; Length 443;
Best Local Similarity 26.9%; Pred. No. 2.3e+02;
RESULT 429
ID AAU28084 standard; protein; 529 AA.
DE Novel human secretory protein, Seq ID No 253.
PN WO200166689-A2.
PD 13-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match Similarity 6.9%; Score 72; DB 4; Length 529;
Best Local Similarity 24.2%; Pred. No. 3e+02;
RESULT 430
ID ABP69048 standard; protein; 642 AA.
DE Human polypeptide SEQ ID NO 1095.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match Similarity 6.9%; Score 72; DB 5; Length 642;
Best Local Similarity 22.2%; Pred. No. 3.9e+02;
RESULT 431
ID ABM80543 standard; protein; 647 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO81111, SEQ:1381.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match Similarity 6.9%; Score 72; DB 8; Length 647;
Best Local Similarity 22.1%; Pred. No. 3.9e+02;
RESULT 432
ID ABB97340 standard; protein; 714 AA.
DE Novel human protein SEQ ID NO: 608.
PN WO200222660-A2.
PD 21-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match Similarity 6.9%; Score 72; DB 5; Length 714;
Best Local Similarity 21.3%; Pred. No. 4.5e+02;
RESULT 433
ID ABM80542 standard; protein; 802 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO81110, SEQ:1379.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match Similarity 6.9%; Score 72; DB 8; Length 802;
Best Local Similarity 22.1%; Pred. No. 5.2e+02;
RESULT 434
ID ABB60137 standard; protein; 1042 AA.

DE Drosophila melanogaster polypeptide SEQ ID NO 7203.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match Similarity 6.9%; Score 72; DB 4; Length 1042;
Best Local Similarity 26.4%; Pred. No. 7.5e+02;
RESULT 435
ID ABB62029 standard; protein; 1102 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 12879.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match Similarity 6.9%; Score 72; DB 4; Length 1102;
Best Local Similarity 26.4%; Pred. No. 8.1e+02;
RESULT 436
ID ADO19681 standard; protein; 1365 AA.
DE Human PRO polypeptide #304.
PN WO2004043361-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match Similarity 6.9%; Score 72; DB 8; Length 1365;
Best Local Similarity 22.1%; Pred. No. 1.1e+03;
RESULT 437
ID ABM80541 standard; protein; 1365 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO81109, SEQ:1377.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match Similarity 6.9%; Score 72; DB 8; Length 1365;
Best Local Similarity 22.1%; Pred. No. 1.1e+03;
RESULT 438
ID ADP24189 standard; protein; 1365 AA.
DE PRO polypeptide SEQ ID NO:1367.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match Similarity 6.9%; Score 72; DB 8; Length 1365;
Best Local Similarity 22.1%; Pred. No. 1.1e+03;
RESULT 439
ID ABO60418 standard; protein; 211 AA.
DE Human genome derived single exon protein #6652.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match Similarity 6.9%; Score 71.5; DB 8; Length 211;
Best Local Similarity 24.2%; Pred. No. 95;
RESULT 440
ID ADP22544 standard; protein; 216 AA.
DE Sea-squirt (Ciona intestinalis) zinc finger protein #59.
PN JP2004057126-A.
PD 26-FEB-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match Similarity 6.9%; Score 71.5; DB 8; Length 216;
Best Local Similarity 23.2%; Pred. No. 98;
RESULT 441
ID ADS23054 standard; protein; 376 AA.
DE Bacterial polypeptide #12087.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match Similarity 6.9%; Score 71.5; DB 8; Length 376;
Best Local Similarity 24.3%; Pred. No. 2.1e+02;
RESULT 442
ID ABP65948 standard; protein; 450 AA.
DE Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:692.
PN EPI227152-A1.
PD 31-JUL-2002.

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PA (NEST ) SOC PROD NESTLE SA.
Query Match 6.9%; Score 71.5; DB 5; Length 450;
Best Local Similarity 19.4%; Pred. No. 2.7e+02;
RESULT 443
ID ABB65496 standard; protein; 456 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 23280.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 6.9%; Score 71.5; DB 4; Length 456;
Best Local Similarity 20.1%; Pred. No. 2.7e+02;
RESULT 444
ID ADN99837 standard; protein; 487 AA.
DE Novel human protein sequence #653.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 6.9%; Score 71.5; DB 8; Length 487;
Best Local Similarity 24.5%; Pred. No. 3e+02;
RESULT 445
ID ABO84713 standard; protein; 524 AA.
DE Human cancer-associated protein HP21-032.6.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 6.9%; Score 71.5; DB 8; Length 524;
Best Local Similarity 22.4%; Pred. No. 3.3e+02;
RESULT 446
ID AAW27598 standard; protein; 556 AA.
DE Human fibulin type 1 isoform (variant A).
PN WO9738014-A1.
PD 16-OCT-1997.
PA (AMGE-) AMGEN INC.
Query Match 6.9%; Score 71.5; DB 2; Length 556;
Best Local Similarity 22.4%; Pred. No. 3.6e+02;
RESULT 447
ID ABO84709 standard; protein; 559 AA.
DE Human cancer-associated protein HP21-032.2.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 6.9%; Score 71.5; DB 8; Length 559;
Best Local Similarity 22.4%; Pred. No. 3.6e+02;
RESULT 448
ID AAR1148 standard; protein; 566 AA.
DE Fibulin A.
PN WO9102755-A.
PD 07-MAR-1991.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
PA (AMNA-) AMER NAT RED CROSS.
Query Match 6.9%; Score 71.5; DB 2; Length 566;
Best Local Similarity 22.4%; Pred. No. 3.7e+02;
RESULT 449
ID AA15574 standard; protein; 566 AA.
DE Human fibulin-1A protein.
PN WO200189548-A2.
PD 29-NOV-2001.
PA (SCHD ) SCHERING AG.
PA (UYNC-) UNIV NORTH CAROLINA.
Query Match 6.9%; Score 71.5; DB 5; Length 566;
Best Local Similarity 22.4%; Pred. No. 3.7e+02;
RESULT 450
ID ADN03779 standard; protein; 566 AA.
DE Antiporiatric protein sequence #86.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match 6.9%; Score 71.5; DB 8; Length 566;
Best Local Similarity 22.4%; Pred. No. 3.7e+02;
RESULT 451
ID ABO84714 standard; protein; 566 AA.
DE Human cancer-associated protein HP21-032.7.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 6.9%; Score 71.5; DB 8; Length 566;
Best Local Similarity 22.4%; Pred. No. 3.7e+02;
RESULT 452
ID ABO84710 standard; protein; 581 AA.
DE Human cancer-associated protein HP21-032.3.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 6.9%; Score 71.5; DB 8; Length 581;
Best Local Similarity 22.4%; Pred. No. 3.8e+02;
RESULT 453
ID AAO30833 standard; protein; 596 AA.
DE Human cell adhesion and extracellular matrix protein (CADECM)-23.
PN WO2003047526-A2.
PD 12-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.9%; Score 71.5; DB 7; Length 596;
Best Local Similarity 22.4%; Pred. No. 3.9e+02;
RESULT 454
ID AAR1149 standard; protein; 601 AA.
DE Fibulin B.
PN WO9102755-A.
PD 07-MAR-1991.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
PA (AMNA-) AMER NAT RED CROSS.
Query Match 6.9%; Score 71.5; DB 2; Length 601;
Best Local Similarity 22.4%; Pred. No. 4e+02;
RESULT 455
ID AAW27599 standard; protein; 601 AA.
DE Human fibulin type 1 isoform (variant B).
PN WO9738014-A1.
PD 16-OCT-1997.
PA (AMGE-) AMGEN INC.
Query Match 6.9%; Score 71.5; DB 2; Length 601;
Best Local Similarity 22.4%; Pred. No. 4e+02;
RESULT 456
ID AA15575 standard; protein; 601 AA.
DE Human fibulin-1B protein.
PN WO200189548-A2.
PD 29-NOV-2001.
PA (SCHD ) SCHERING AG.
PA (UYNC-) UNIV NORTH CAROLINA.
Query Match 6.9%; Score 71.5; DB 5; Length 601;
Best Local Similarity 22.4%; Pred. No. 4e+02;
RESULT 457
ID ABO84717 standard; protein; 601 AA.
DE Human cancer-associated protein HP21-032.10.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 6.9%; Score 71.5; DB 8; Length 601;
Best Local Similarity 22.4%; Pred. No. 4e+02;
RESULT 458
ID ABO84258 standard; protein; 622 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4507.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.9%; Score 71.5; DB 8; Length 622;
Best Local Similarity 22.4%; Pred. No. 4.2e+02;
RESULT 459
ID ABO84259 standard; protein; 622 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4508.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.9%; Score 71.5; DB 8; Length 622;
Best Local Similarity 22.4%; Pred. No. 4.2e+02;
RESULT 460
ID ABB72020 standard; protein; 631 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 42852.
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PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.9%; Score 71.5; DB 4; Length 631;
Best Local Similarity 19.9%; Pred. No. 4.2e+02;
RESULT 461
ID ADB64295 standard; protein; 636 AA.
DE Human protein encoded by clone FCBBF30021900.
PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
Query Match 6.9%; Score 71.5; DB 7; Length 636;
Best Local Similarity 22.6%; Pred. No. 4.3e+02;
RESULT 462
ID ABM84261 standard; protein; 636 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4510.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.9%; Score 71.5; DB 8; Length 636;
Best Local Similarity 22.4%; Pred. No. 4.3e+02;
RESULT 463
ID ABP62984 standard; protein; 641 AA.
DE Human polypeptide SEQ ID NO 421.
PN WO200218424-A2.
PD 07-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 6.9%; Score 71.5; DB 5; Length 641;
Best Local Similarity 20.2%; Pred. No. 4.3e+02;
RESULT 464
ID ABO84712 standard; protein; 641 AA.
DE Human cancer-associated protein HP21-032.5.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 6.9%; Score 71.5; DB 8; Length 641;
Best Local Similarity 22.4%; Pred. No. 4.3e+02;
RESULT 465
ID ADD26679 standard; protein; 653 AA.
DE Human adipocyte bait protein fibulin 1C (FBLN1).
PN WO200290544-A2.
PD 14-NOV-2002.
PA (HYBR-) HYBRIGENICS.
PA (LYNX-) LYNX THERAPEUTICS INC.
Query Match 6.9%; Score 71.5; DB 7; Length 653;
Best Local Similarity 22.4%; Pred. No. 4.4e+02;
RESULT 466
ID ABO84708 standard; protein; 661 AA.
DE Human cancer-associated protein HP21-032.1.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 6.9%; Score 71.5; DB 8; Length 661;
Best Local Similarity 22.4%; Pred. No. 4.5e+02;
RESULT 467
ID AAR1150 standard; protein; 683 AA.
DE Fibulin C.
PN WO9102755-A.
PD 07-MAR-1991.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
PA (AMNA-) AMER NAT RED CROSS.
Query Match 6.9%; Score 71.5; DB 2; Length 683;
Best Local Similarity 22.4%; Pred. No. 4.7e+02;
RESULT 468
ID AAW27600 standard; protein; 683 AA.
DE Human fibulin type 1 isoform (variant C).
PN WO9738014-A1.
PD 16-OCT-1997.
PA (AMGE-) AMGEN INC.
Query Match 6.9%; Score 71.5; DB 2; Length 683;
Best Local Similarity 22.4%; Pred. No. 4.7e+02;
RESULT 469
ID AAE15576 standard; protein; 683 AA.
DE Human fibulin-1AC protein.
PN WO200189548-A2.
PD 29-NOV-2001.
PA (SCHD) SCHERING AG.
PA (UNYC-) UNIV NORTH CAROLINA.
Query Match 6.9%; Score 71.5; DB 5; Length 683;
Best Local Similarity 22.4%; Pred. No. 4.7e+02;
RESULT 470
ID ABO84716 standard; protein; 683 AA.
DE Human cancer-associated protein HP21-032.9.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 6.9%; Score 71.5; DB 8; Length 683;
Best Local Similarity 22.4%; Pred. No. 4.7e+02;
RESULT 471
ID ABG19385 standard; protein; 686 AA.
DE Novel human diagnostic protein #19376.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.9%; Score 71.5; DB 4; Length 686;
Best Local Similarity 22.4%; Pred. No. 4.8e+02;
RESULT 472
ID ABO84711 standard; protein; 698 AA.
DE Human cancer-associated protein HP21-032.4.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 6.9%; Score 71.5; DB 8; Length 698;
Best Local Similarity 22.4%; Pred. No. 4.9e+02;
RESULT 473
ID AAW27601 standard; protein; 703 AA.
DE Human fibulin type 1 isoform (variant D).
PN WO9738014-A1.
PD 16-OCT-1997.
PA (AMGE-) AMGEN INC.
Query Match 6.9%; Score 71.5; DB 2; Length 703;
Best Local Similarity 22.4%; Pred. No. 4.9e+02;
RESULT 474
ID AAE15577 standard; protein; 703 AA.
DE Human fibulin-1D protein.
PN WO200189548-A2.
PD 29-NOV-2001.
PA (SCHD) SCHERING AG.
PA (UNYC-) UNIV NORTH CAROLINA.
Query Match 6.9%; Score 71.5; DB 5; Length 703;
Best Local Similarity 22.4%; Pred. No. 4.9e+02;
RESULT 475
ID ADN03922 standard; protein; 703 AA.
DE Antiprosoriatic protein sequence #156.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 6.9%; Score 71.5; DB 8; Length 703;
Best Local Similarity 22.4%; Pred. No. 4.9e+02;
RESULT 476
ID ABO84715 standard; protein; 703 AA.
DE Human cancer-associated protein HP21-032.8.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 6.9%; Score 71.5; DB 8; Length 703;
Best Local Similarity 22.4%; Pred. No. 4.9e+02;
RESULT 477
ID ADT49905 standard; protein; 703 AA.
DE Human FBLN1 SEQ ID NO:112.
PN WO2004083241-A2.
PD 30-SEP-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 6.9%; Score 71.5; DB 8; Length 703;
Best Local Similarity 22.4%; Pred. No. 4.9e+02;

RESULT 478
ID ABG19386 standard; protein; 706 AA.
DE Novel human diagnostic protein #19377.
FN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.9%; Score 71.5; DB 4; Length 706;
Best Local Similarity 22.4%; Pred. No. 5e+02;
RESULT 479
ID AAM38820 standard; protein; 743 AA.
DE Human polypeptide SEQ ID NO 1965.
FN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.9%; Score 71.5; DB 4; Length 743;
Best Local Similarity 24.5%; Pred. No. 5.3e+02;
RESULT 480
ID AAM40606 standard; protein; 795 AA.
DE Human polypeptide SEQ ID NO 5537.
FN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.9%; Score 71.5; DB 4; Length 795;
Best Local Similarity 24.5%; Pred. No. 5.8e+02;
RESULT 481
ID ADP25097 standard; protein; 799 AA.
DE PRO polypeptide SEQ ID NO:2275.
FN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH-) GENENTECH INC.
Query Match 6.9%; Score 71.5; DB 8; Length 799;
Best Local Similarity 24.5%; Pred. No. 5.9e+02;
RESULT 482
ID ADJ69061 standard; protein; 1300 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID867.
FN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 6.9%; Score 71.5; DB 7; Length 1300;
Best Local Similarity 23.7%; Pred. No. 1.1e+03;
RESULT 483
ID ABG15511 standard; protein; 1907 AA.
DE Novel human diagnostic protein #15502.
FN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.9%; Score 71.5; DB 4; Length 1907;
Best Local Similarity 24.5%; Pred. No. 1.9e+03;
RESULT 484
ID AAY93724 standard; protein; 139 AA.
DE The kappa chain of immunoglobulin clone 12.3.1.1.
FN WO200037504-A2.
PD 29-JUN-2000.
PA (PFIZ-) PFIZER INC.
PA (ABGE-) AGENIX INC.
Query Match 6.9%; Score 71; DB 3; Length 139;
Best Local Similarity 24.1%; Pred. No. 60;
RESULT 485
ID AAE35908 standard; protein; 139 AA.
DE Human 12.3.1 anti-CTLA-4 antibody kappa chain.
FN EP1262193-A1.
PD 04-DEC-2002.
PA (PFIZ-) PFIZER PROD INC.
Query Match 6.9%; Score 71; DB 6; Length 139;
Best Local Similarity 24.1%; Pred. No. 60;
RESULT 486
ID AAG63949 standard; protein; 164 AA.
DE Human prostate cancer associated antigen protein sequence SEQ ID NO:1311.
FN WO200073801-A2.
PD 07-DEC-2000.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match 6.9%; Score 71; DB 4; Length 164;

Best Local Similarity 33.8%; Pred. No. 76;
RESULT 487
ID ABB57214 standard; protein; 193 AA.
DE Mouse ischaemic condition related protein sequence SEQ ID NO:520.
FN WO200188188-A2.
PD 22-NOV-2001.
PA (UVNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
Query Match 6.9%; Score 71; DB 5; Length 193;
Best Local Similarity 20.5%; Pred. No. 94;
RESULT 488
ID AAG10021 standard; protein; 195 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 8177.
FN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.9%; Score 71; DB 3; Length 195;
Best Local Similarity 26.6%; Pred. No. 96;
RESULT 489
ID AAY68994 standard; protein; 219 AA.
DE Amino acid sequence of light chain of anti-delta9-desaturase antibody.
FN WO200005391-A1.
PD 03-FEB-2000.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 6.9%; Score 71; DB 3; Length 219;
Best Local Similarity 23.8%; Pred. No. 1.1e+02;
RESULT 490
ID ASP58286 standard; protein; 219 AA.
DE Humanised 10D5 antibody light chain.
FN WO200288307-A2.
PD 07-NOV-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 6.9%; Score 71; DB 6; Length 219;
Best Local Similarity 23.8%; Pred. No. 1.1e+02;
RESULT 491
ID ABP58288 standard; protein; 238 AA.
DE Humanised 10D5 antibody light chain.
FN WO200288307-A2.
PD 07-NOV-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 6.9%; Score 71; DB 6; Length 238;
Best Local Similarity 23.8%; Pred. No. 1.3e+02;
RESULT 492
ID AAM16561 standard; protein; 284 AA.
DE Peptide #2995 encoded by probe for measuring cervical gene expression.
FN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.9%; Score 71; DB 4; Length 284;
Best Local Similarity 21.0%; Pred. No. 1.6e+02;
RESULT 493
ID ABB35545 standard; peptide; 284 AA.
DE Peptide #3051 encoded by human foetal liver single exon probe.
FN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.9%; Score 71; DB 4; Length 284;
Best Local Similarity 21.0%; Pred. No. 1.6e+02;
RESULT 494
ID AAM29045 standard; protein; 284 AA.
DE Peptide #3082 encoded by probe for measuring placental gene expression.
FN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.9%; Score 71; DB 4; Length 284;
Best Local Similarity 21.0%; Pred. No. 1.6e+02;
RESULT 495
ID ABB30371 standard; peptide; 284 AA.
DE Peptide #3022 encoded by breast cell single exon nucleic acid probe.
FN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.9%; Score 71; DB 4; Length 284;
Best Local Similarity 21.0%; Pred. No. 1.6e+02;
RESULT 496

ID ABB20970 standard; protein; 284 AA.
DE Protein #2969 encoded by probe for measuring heart cell gene expression.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.9%; Score 71; DB 4; Length 284;
Best Local Similarity 21.0%; Pred. No. 1.6e+02;
RESULT 497
ID AAM68734 standard; protein; 284 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 29040.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.9%; Score 71; DB 4; Length 284;
Best Local Similarity 21.0%; Pred. No. 1.6e+02;
RESULT 498
ID AAM56359 standard; protein; 284 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 28464.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.9%; Score 71; DB 4; Length 284;
Best Local Similarity 21.0%; Pred. No. 1.6e+02;
RESULT 499
ID ABG50404 standard; peptide; 284 AA.
DE Human liver peptide, SEQ ID NO 29052.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.9%; Score 71; DB 4; Length 284;
Best Local Similarity 21.0%; Pred. No. 1.6e+02;
RESULT 500
ID AAM4274 standard; protein; 284 AA.
DE Peptide #2956 encoded by probe for measuring breast gene expression.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.9%; Score 71; DB 4; Length 284;
Best Local Similarity 21.0%; Pred. No. 1.6e+02;
RESULT 501
ID ABG38320 standard; peptide; 284 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 27985.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.9%; Score 71; DB 5; Length 284;
Best Local Similarity 21.0%; Pred. No. 1.6e+02;
RESULT 502
ID ADJ76243 standard; protein; 332 AA.
DE Marker gene related amino acid sequence SEQ ID NO:1495.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 6.9%; Score 71; DB 8; Length 332;
Best Local Similarity 22.5%; Pred. No. 2e+02;
RESULT 503
ID AAB95493 standard; protein; 426 AA.
DE Human protein sequence SEQ ID NO:18033.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 6.9%; Score 71; DB 4; Length 426;
Best Local Similarity 21.0%; Pred. No. 2.8e+02;
RESULT 504
ID ADJ69991 standard; protein; 426 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1797.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 6.9%; Score 71; DB 7; Length 426;
Best Local Similarity 21.0%; Pred. No. 2.8e+02;
RESULT 505

ID ADN9893 standard; protein; 459 AA.
DE Novel human protein sequence #709.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 6.9%; Score 71; DB 8; Length 459;
Best Local Similarity 20.8%; Pred. No. 3.1e+02;
RESULT 506
ID ADJ95136 standard; protein; 524 AA.
DE Novel NOVX protein sequence #182.
PN WO2003040325-A2.
PD 15-MAY-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.9%; Score 71; DB 7; Length 524;
Best Local Similarity 21.1%; Pred. No. 3.7e+02;
RESULT 507
ID ADJ95134 standard; protein; 524 AA.
DE Novel NOVX protein sequence #181.
PN WO2003040325-A2.
PD 15-MAY-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.9%; Score 71; DB 7; Length 524;
Best Local Similarity 21.1%; Pred. No. 3.7e+02;
RESULT 508
ID ADJ75681 standard; protein; 524 AA.
DE Marker gene related amino acid sequence SEQ ID NO:933.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 6.9%; Score 71; DB 8; Length 524;
Best Local Similarity 21.1%; Pred. No. 3.7e+02;
RESULT 509
ID ADN04293 standard; protein; 524 AA.
DE Antiporiatic protein sequence #341.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 6.9%; Score 71; DB 8; Length 524;
Best Local Similarity 21.1%; Pred. No. 3.7e+02;
RESULT 510
ID ADP24028 standard; protein; 524 AA.
DE PRO polypeptide SEQ ID NO:1206.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 6.9%; Score 71; DB 8; Length 524;
Best Local Similarity 21.1%; Pred. No. 3.7e+02;
RESULT 511
ID ADJ95132 standard; protein; 536 AA.
DE Novel NOVX protein sequence #180.
PN WO2003040325-A2.
PD 15-MAY-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.9%; Score 71; DB 7; Length 536;
Best Local Similarity 21.1%; Pred. No. 3.8e+02;
RESULT 512
ID ADJ95130 standard; protein; 552 AA.
DE Novel NOVX protein sequence #179.
PN WO2003040325-A2.
PD 15-MAY-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.9%; Score 71; DB 7; Length 552;
Best Local Similarity 21.1%; Pred. No. 4e+02;
RESULT 513
ID ADJ69512 standard; protein; 553 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1318.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 6.9%; Score 71; DB 7; Length 553;
Best Local Similarity 21.1%; Pred. No. 4e+02;
RESULT 514

ID ABJ37100 standard; protein; 628 AA.
DE Concatameric immunoadhesion human protein sequence SEQ ID NO 6.
PN WO2003010202-A1.
PD 06-FEB-2003.
PA (MEDE-) MEDEXGEN CO LTD.
Query Match 6.9%; Score 71; DB 6; Length 628;
Best Local Similarity 22.4%; Pred. No. 4.8e+02;
RESULT 515
ID ADQ79904 standard; protein; 628 AA.
DE Human tumour necrosis factor receptor 1, TNFR1-TNFR1/Ig construct.
PN KR2004009997-A.
PD 31-JAN-2004.
PA (MEDE-) MEDEXGEN INC.
Query Match 6.9%; Score 71; DB 8; Length 628;
Best Local Similarity 22.4%; Pred. No. 4.8e+02;
RESULT 516
ID ABB57783 standard; protein; 657 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 141.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.9%; Score 71; DB 4; Length 657;
Best Local Similarity 23.4%; Pred. No. 5.1e+02;
RESULT 517
ID AD52670 standard; protein; 967 AA.
DE Human protein SEQ ID 36.
PN WO2003089466-A1.
PD 30-OCT-2003.
PA (RIKE) RIKEN KK.
PA (DNAF-) DNAFORM KK.
PA (MITU) MITSUBISHI CHEM CORP.
Query Match 6.9%; Score 71; DB 8; Length 967;
Best Local Similarity 26.2%; Pred. No. 8.6e+02;
RESULT 518
ID ABG08492 standard; protein; 974 AA.
DE Novel human diagnostic protein #8483.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.9%; Score 71; DB 4; Length 974;
Best Local Similarity 21.9%; Pred. No. 8.7e+02;
RESULT 519
ID ADF75895 standard; protein; 1121 AA.
DE Acidothermus cellulolyticus Gux1 protein.
PN US2003096342-A1.
PD 22-MAY-2003.
PA (ADNE/) ADNEY W S.
PA (DING/) DING S.
PA (VINZ/) VINZANT T B.
PA (HMM/) HIMMEL M E.
PA (DECK/) DECKER S R.
PA (MCCA/) MCCARTER S L.
Query Match 6.9%; Score 71; DB 7; Length 1121;
Best Local Similarity 21.4%; Pred. No. 1.1e+03;
RESULT 520
ID AAG38482 standard; protein; 1517 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 47481.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.9%; Score 71; DB 3; Length 1517;
Best Local Similarity 25.6%; Pred. No. 1.6e+03;
RESULT 521
ID AAG38481 standard; protein; 1543 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 47480.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.9%; Score 71; DB 3; Length 1543;
Best Local Similarity 25.6%; Pred. No. 1.6e+03;
RESULT 522
ID AAG38480 standard; protein; 1672 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 47479.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.9%; Score 71; DB 3; Length 1672;
Best Local Similarity 25.6%; Pred. No. 1.8e+03;
RESULT 523
ID ADB79961 standard; protein; 3262 AA.
DE Mouse serine/threonine protein kinase SEQ ID NO: 4.
PN WO2003076577-A2.
PD 18-SEP-2003.
PA (APPL-) APPLERA CORP.
Query Match 6.9%; Score 71; DB 7; Length 3262;
Best Local Similarity 27.9%; Pred. No. 4.5e+03;
RESULT 524
ID ABB70878 standard; protein; 3680 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 39426.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.9%; Score 71; DB 4; Length 3680;
Best Local Similarity 22.4%; Pred. No. 5.3e+03;
RESULT 525
ID AAG08697 standard; protein; 276 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 6337.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.8%; Score 70.5; DB 3; Length 276;
Best Local Similarity 20.8%; Pred. No. 1.7e+02;
RESULT 526
ID ADM80106 standard; protein; 330 AA.
DE Spiramycin biosynthesis orf19 protein, SEQ ID 73.
PN FR2845394-A1.
PD 09-APR-2004.
PA (AVET) AVENTIS PHARMA SA.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.8%; Score 70.5; DB 8; Length 330;
Best Local Similarity 21.7%; Pred. No. 2.2e+02;
RESULT 527
ID ADN97622 standard; protein; 330 AA.
DE S ambofaciens spiramycin biosynthetic enzyme encoded by ORF19.
PN WO2004033689-A2.
PD 22-APR-2004.
PA (AVET) AVENTIS PHARMA SA.
PA (CNRS) CNRS.
Query Match 6.8%; Score 70.5; DB 8; Length 330;
Best Local Similarity 21.7%; Pred. No. 2.2e+02;
RESULT 528
ID ADM04511 standard; protein; 359 AA.
DE Human protein of the invention SEQ ID NO: 3196.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.8%; Score 70.5; DB 7; Length 359;
Best Local Similarity 26.7%; Pred. No. 2.5e+02;
RESULT 529
ID ADD84887 standard; protein; 392 AA.
DE Bacillus amyloliquefaciens subtilisin protein #1.
PN WO2003062380-A2.
PD 31-JUL-2003.
PA (GEMV) GENENCOR INT INC.
Query Match 6.8%; Score 70.5; DB 7; Length 392;
Best Local Similarity 21.3%; Pred. No. 2.8e+02;
RESULT 530
ID AAU38518 standard; protein; 393 AA.
DE B. amyloliquefaciens subtilisin (BPN).
PN WO200159130-A2.
PD 16-AUG-2001.
PA (GEMV) GENENCOR INT INC.
Query Match 6.8%; Score 70.5; DB 4; Length 393;
Best Local Similarity 21.3%; Pred. No. 2.8e+02;
RESULT 531
ID ADB65521 standard; protein; 428 AA.
DE Human protein encoded by clone TESTI20282530.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.8%; Score 70.5; DB 7; Length 428;
Best Local Similarity 22.2%; Pred. No. 3.2e+02;
RESULT 532
ID ABP96244 standard; protein; 429 AA.
DE Human nucleic-acid associated protein 27 SEQ ID NO:27.
PN WO2003016549-A2.
PD 27-FEB-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.8%; Score 70.5; DB 6; Length 429;
Best Local Similarity 26.7%; Pred. No. 3.2e+02;
RESULT 533
ID ADJ37221 standard; protein; 430 AA.
DE Human nucleic-acid associated protein NAAP-10 SEQ ID NO:10.
PN WO2004011604-A2.
PD 05-FEB-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.8%; Score 70.5; DB 8; Length 430;
Best Local Similarity 26.7%; Pred. No. 3.2e+02;
RESULT 534
ID ADM87363 standard; protein; 430 AA.
DE Human protein SEQ ID NO:456.
PN WO2004009834-A2.
PD 29-JAN-2004.
PA (NUVE-) NUVELO INC.
Query Match 6.8%; Score 70.5; DB 8; Length 430;
Best Local Similarity 26.7%; Pred. No. 3.2e+02;
RESULT 535
ID ABG20141 standard; protein; 524 AA.
DE Novel human diagnostic protein #20132.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.8%; Score 70.5; DB 4; Length 524;
Best Local Similarity 25.9%; Pred. No. 4.2e+02;
RESULT 536
ID ADN95533 standard; protein; 572 AA.
DE Novel human protein sequence #349.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 6.8%; Score 70.5; DB 8; Length 572;
Best Local Similarity 20.2%; Pred. No. 4.7e+02;
RESULT 537
ID AAY34517 standard; protein; 670 AA.
DE Porphyromonas gingivalis protein PG55.
PN WO9929870-A1.
PD 17-JUN-1999.
PA (CSLC-) CSL LTD.
Query Match 6.8%; Score 70.5; DB 2; Length 670;
Best Local Similarity 26.1%; Pred. No. 5.9e+02;
RESULT 538
ID AAY34390 standard; protein; 702 AA.
DE Porphyromonas gingivalis protein PG55.
PN WO9529870-A1.
PD 17-JUN-1999.
PA (CSLC-) CSL LTD.
Query Match 6.8%; Score 70.5; DB 2; Length 702;
Best Local Similarity 26.1%; Pred. No. 6.2e+02;
RESULT 539
ID AAU20496 standard; protein; 705 AA.
DE Human secreted protein, Seq ID No 488.
PN WO200155326-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.8%; Score 70.5; DB 4; Length 705;
Best Local Similarity 26.8%; Pred. No. 6.3e+02;
RESULT 540
ID AAB33788 standard; protein; 909 AA.
DE Human nucleic acid associated protein (NAAP)-28.
PN WO200299115-A2.
PD 12-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
PA (YUEH/) YUE H.
Query Match 6.8%; Score 70.5; DB 6; Length 909;
Best Local Similarity 22.2%; Pred. No. 8.9e+02;
RESULT 541
ID ABB66060 standard; protein; 1449 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 24972.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.8%; Score 70.5; DB 4; Length 1449;
Best Local Similarity 21.4%; Pred. No. 1.7e+03;
RESULT 542
ID ADD48744 standard; protein; 1468 AA.
DE Rat Protein P49791, SEQ ID NO 14453.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.8%; Score 70.5; DB 7; Length 1468;
Best Local Similarity 21.1%; Pred. No. 1.7e+03;
RESULT 543
ID AAY33730 standard; protein; 1481 AA.
DE Phototaxobius luminescens 1481 amino acid insecticidal toxin.
PN WO9942589-A2.
PD 26-AUG-1999.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
Query Match 6.8%; Score 70.5; DB 2; Length 1481;
Best Local Similarity 25.1%; Pred. No. 1.7e+03;
RESULT 544
ID ABU42513 standard; protein; 1633 AA.
DE Protein encoded by Prokaryotic essential gene #28040.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.8%; Score 70.5; DB 6; Length 1633;
Best Local Similarity 23.2%; Pred. No. 2e+03;
RESULT 545
ID AAY83170 standard; protein; 1802 AA.
DE Cell wall protein SdrF.
PN WO200012689-A1.
PD 09-MAR-2000.
PA (QUEE-) QUEEN ELIZABETH COLLEGE DUBLIN.
PA (TEXA) UNIV TEXAS A & M SYSTEM.
Query Match 6.8%; Score 70.5; DB 3; Length 1802;
Best Local Similarity 23.2%; Pred. No. 2.3e+03;
RESULT 546
ID AAY70119 standard; protein; 1802 AA.
DE Staph. epidermidis serine-aspartate repeat region protein SdrF.
PN WO200012131-A1.
PD 09-MAR-2000.
PA (INHI-) INHIBITEX INC.
PA (TEXA) UNIV TEXAS A & M SYSTEM.
PA (QUEE-) QUEEN ELIZABETH COLLEGE DUBLIN.
Query Match 6.8%; Score 70.5; DB 3; Length 1802;
Best Local Similarity 23.2%; Pred. No. 2.3e+03;
RESULT 547
ID AAG01884 standard; protein; 155 AA.
DE Human secreted protein, SEQ ID NO: 5965.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 6.8%; Score 70; DB 3; Length 155;
Best Local Similarity 35.3%; Pred. No. 89;
RESULT 548
ID ADI15668 standard; protein; 164 AA.
DE Partial murine antibody B436 light (kappa) chain protein SeqID 42.
PN WO2004018997-A2.
PD 04-MAR-2004.
PA (NEUR-) NEUROGENETICS INC.
Query Match 6.8%; Score 70; DB 8; Length 164;
Best Local Similarity 23.4%; Pred. No. 96;
RESULT 549

ID ADL15642 standard; protein; 164 AA.
DE Murine antibody B436 light (kappa) chain protein SeqID 16.
PN WO2004018997-A2.
PD 04-MAR-2004.
PA (NEUR-) NEUROGENETICS INC.
Query Match 6.8%; Score 70; DB 8; Length 164;
Best Local Similarity 23.4%; Pred. No. 96;
RESULT 550
ID ABB64175 standard; protein; 179 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 19317.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.8%; Score 70; DB 4; Length 179;
Best Local Similarity 25.9%; Pred. No. 1.1e+02;
RESULT 551
ID AAB36373 standard; protein; 193 AA.
DE Rat CRP protein sequence SEQ ID NO:9.
PN WO200066734-A1.
PD 09-NOV-2000.
PA (HARD) HARVARD COLLEGE.
Query Match 6.8%; Score 70; DB 3; Length 193;
Best Local Similarity 20.5%; Pred. No. 1.2e+02;
RESULT 552
ID ADQ82998 standard; protein; 193 AA.
DE Rat CRP1, SEQ ID 4.
PN WO2004062474-A2.
PD 29-JUL-2004.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
Query Match 6.8%; Score 70; DB 8; Length 193;
Best Local Similarity 20.5%; Pred. No. 1.2e+02;
RESULT 553
ID ADL15725 standard; protein; 219 AA.
DE Murine antibody B436 light (kappa) chain protein SeqID 99.
PN WO2004018997-A2.
PD 04-MAR-2004.
PA (NEUR-) NEUROGENETICS INC.
Query Match 6.8%; Score 70; DB 8; Length 219;
Best Local Similarity 23.4%; Pred. No. 1.4e+02;
RESULT 554
ID AAB21000 standard; protein; 255 AA.
DE Human nucleic acid-binding protein, NuABP-4.
PN WO200044900-A2.
PD 03-AUG-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 6.8%; Score 70; DB 3; Length 255;
Best Local Similarity 23.7%; Pred. No. 1.8e+02;
RESULT 555
ID AAG42638 standard; protein; 294 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 53198.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (MENND-) MENDEL BIOTECHNOLOGY INC.
Query Match 6.8%; Score 70; DB 3; Length 294;
Best Local Similarity 20.1%; Pred. No. 2.1e+02;
RESULT 556
ID ADQ61841 standard; protein; 294 AA.
DE Transcription factor G1917, SEQ ID 308.
PN WO2004031349-A2.
PD 15-APR-2004.
PA (MENND-) MENDEL BIOTECHNOLOGY INC.
Query Match 6.8%; Score 70; DB 8; Length 294;
Best Local Similarity 20.1%; Pred. No. 2.1e+02;
RESULT 557
ID AAG42637 standard; protein; 295 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 53197.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (MENND-) MENDEL BIOTECHNOLOGY INC.
Query Match 6.8%; Score 70; DB 3; Length 295;
Best Local Similarity 20.1%; Pred. No. 2.1e+02;
RESULT 558
ID ABP51373 standard; protein; 298 AA.
DE Human MDDT SEQ ID NO 395.
PN WO200240715-A2.

PD 23-MAY-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.8%; Score 70; DB 5; Length 298;
Best Local Similarity 23.7%; Pred. No. 2.2e+02;
RESULT 559
ID ABG17131 standard; protein; 307 AA.
DE Novel human diagnostic protein #17122.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.8%; Score 70; DB 4; Length 307;
Best Local Similarity 24.9%; Pred. No. 2.3e+02;
RESULT 560
ID ABG06645 standard; protein; 335 AA.
DE Novel human diagnostic protein #6636.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.8%; Score 70; DB 4; Length 335;
Best Local Similarity 20.2%; Pred. No. 2.6e+02;
RESULT 561
ID ABR41451 standard; protein; 369 AA.
DE Human DITHP zinc finger transcriptional regulator.
PN WO200297031-A2.
PD 05-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.8%; Score 70; DB 6; Length 369;
Best Local Similarity 24.8%; Pred. No. 2.9e+02;
RESULT 562
ID AAM39574 standard; protein; 372 AA.
DE Human polypeptide SEQ ID NO 2719.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.8%; Score 70; DB 4; Length 372;
Best Local Similarity 35.3%; Pred. No. 2.9e+02;
RESULT 563
ID ADA54595 standard; protein; 372 AA.
DE Human protein, SEQ ID 2163.
PN EP1293569-A2.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.8%; Score 70; DB 6; Length 372;
Best Local Similarity 35.3%; Pred. No. 2.9e+02;
RESULT 564
ID AAM41360 standard; protein; 376 AA.
DE Human polypeptide SEQ ID NO 6291.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.8%; Score 70; DB 4; Length 376;
Best Local Similarity 35.3%; Pred. No. 3e+02;
RESULT 565
ID ABB59061 standard; protein; 447 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 3975.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.8%; Score 70; DB 4; Length 447;
Best Local Similarity 24.5%; Pred. No. 3.8e+02;
RESULT 566
ID ADM06123 standard; protein; 460 AA.
DE Human protein of the invention SEQ ID NO:4808.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.8%; Score 70; DB 7; Length 460;
Best Local Similarity 19.8%; Pred. No. 3.9e+02;
RESULT 567
ID ABB61007 standard; protein; 468 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 9813.
PN WO200171042-A2.

PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.8%; Score 70; DB 4; Length 468;
Best Local Similarity 24.5%; Pred. No. 4e+02;
RESULT 568
ID ADN99382 standard; protein; 471 AA.
DE Novel human protein sequence #198.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 6.8%; Score 70; DB 8; Length 471;
Best Local Similarity 20.2%; Pred. No. 4.1e+02;
RESULT 569
ID AB096676 standard; protein; 475 AA.
DE Human nucleic acid-associated protein (NAAP) #5.
PN WO2003032003-A2.
PD 20-MAR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.8%; Score 70; DB 6; Length 475;
Best Local Similarity 20.2%; Pred. No. 4.1e+02;
RESULT 570
ID ADJ71120 standard; protein; 553 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID2926.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 6.8%; Score 70; DB 7; Length 553;
Best Local Similarity 21.1%; Pred. No. 5.1e+02;
RESULT 571
ID AB078855 standard; protein; 556 AA.
DE Pseudomonas aeruginosa polypeptide #11030.
PN US651795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.8%; Score 70; DB 7; Length 556;
Best Local Similarity 21.0%; Pred. No. 5.1e+02;
RESULT 572
ID ADC31846 standard; protein; 563 AA.
DE Human novel polypeptide sequence, SEQ ID NO:1928.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 6.8%; Score 70; DB 7; Length 563;
Best Local Similarity 23.7%; Pred. No. 5.2e+02;
RESULT 573
ID AAM79211 standard; protein; 610 AA.
DE Human protein SEQ ID NO 1873.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.8%; Score 70; DB 4; Length 610;
Best Local Similarity 27.2%; Pred. No. 5.8e+02;
RESULT 574
ID AAE33372 standard; protein; 610 AA.
DE Human nucleic acid associated protein (NAAP)-12.
PN WO200299115-A2.
PD 12-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
PA (YUEH/) YUE H.
Query Match 6.8%; Score 70; DB 6; Length 610;
Best Local Similarity 27.2%; Pred. No. 5.8e+02;
RESULT 575
ID ADE56165 standard; protein; 923 AA.
DE Rat Protein D38222, SEQ ID NO 2014.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.8%; Score 70; DB 7; Length 923;
Best Local Similarity 27.4%; Pred. No. 1e+03;
RESULT 576
ID ADD45276 standard; protein; 923 AA.

DE Rat Protein D38222, SEQ ID NO 10709.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.8%; Score 70; DB 7; Length 923;
Best Local Similarity 27.4%; Pred. No. 1e+03;
RESULT 577
ID ABB65792 standard; protein; 1059 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 24168.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.8%; Score 70; DB 4; Length 1059;
Best Local Similarity 21.7%; Pred. No. 1.2e+03;
RESULT 578
ID ABB61539 standard; protein; 1077 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 11409.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.8%; Score 70; DB 4; Length 1077;
Best Local Similarity 21.7%; Pred. No. 1.3e+03;
RESULT 579
ID ABP71656 standard; protein; 1121 AA.
DE A. cellulolyticus Gux1 protein.
PN WO2003012095-A1.
PD 13-FEB-2003.
PA (MIDE) MIDWEST RES INST.
Query Match 6.8%; Score 70; DB 6; Length 1121;
Best Local Similarity 21.5%; Pred. No. 1.3e+03;
RESULT 580
ID ABG15312 standard; protein; 1205 AA.
DE Novel human diagnostic protein #15303.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.8%; Score 70; DB 4; Length 1205;
Best Local Similarity 27.2%; Pred. No. 1.5e+03;
RESULT 581
ID ABG05068 standard; protein; 1205 AA.
DE Novel human diagnostic protein #5059.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.8%; Score 70; DB 4; Length 1205;
Best Local Similarity 27.2%; Pred. No. 1.5e+03;
RESULT 582
ID ABG27121 standard; protein; 1214 AA.
DE Novel human diagnostic protein #27112.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.8%; Score 70; DB 4; Length 1214;
Best Local Similarity 27.2%; Pred. No. 1.5e+03;
RESULT 583
ID ADF11512 standard; protein; 2476 AA.
DE Murine ATRX polypeptide.
PN US2003077800-A1.
PD 24-APR-2003.
PA (HORM-) HORMOS MEDICAL LTD OY.
Query Match 6.8%; Score 70; DB 7; Length 2476;
Best Local Similarity 24.4%; Pred. No. 3.9e+03;
RESULT 584
ID AAR87000 standard; protein; 310 AA.
DE Human syndecan-1.
PN WO9534316-A1.
PD 21-DEC-1995.
PA (JALK/) JALKANEN M.
PA (MALI/) MALI M.
Query Match 6.7%; Score 69.5; DB 2; Length 310;
Best Local Similarity 24.2%; Pred. No. 2.6e+02;
RESULT 585

ID AAW95197 standard; protein; 310 AA.
DE Human syndecan-1.
PN US5851993-A.
PD 22-DEC-1998.
PA (BIOT-) BIOTIE THERAPIES LTD.
Query Match 6.7%; Score 69.5; DB 2; Length 310;
Best Local Similarity 24.2%; Pred. No. 2.6e+02;
RESULT 586
ID ABU07415 standard; protein; 310 AA.
DE Protein differentially regulated in prostate cancer #18.
PN WO200281638-A2.
PD 17-OCT-2002.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match 6.7%; Score 69.5; DB 6; Length 310;
Best Local Similarity 24.2%; Pred. No. 2.6e+02;
RESULT 587
ID ADD67581 standard; protein; 310 AA.
DE Human CD138 protein SEQ ID NO:58.
PN WO2003062401-A2.
PD 31-JUL-2003.
PA (CORI-) CORIXA CORP.
Query Match 6.7%; Score 69.5; DB 7; Length 310;
Best Local Similarity 24.2%; Pred. No. 2.6e+02;
RESULT 588
ID ADJ75822 standard; protein; 310 AA.
DE Marker gene related amino acid sequence SEQ ID NO:774.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 6.7%; Score 69.5; DB 8; Length 310;
Best Local Similarity 24.2%; Pred. No. 2.6e+02;
RESULT 589
ID ADF18675 standard; protein; 310 AA.
DE Human protein encoded by TAT412 cDNA used to treat cancer SeqID 35.
PN WO2004045516-A2.
PD 03-JUN-2004.
PA (GETH-) GENENTECH INC.
Query Match 6.7%; Score 69.5; DB 8; Length 310;
Best Local Similarity 24.2%; Pred. No. 2.6e+02;
RESULT 590
ID ADR68489 standard; protein; 310 AA.
DE Apoptosis-associated polypeptide #1.
PN WO2004072111-A2.
PD 26-AUG-2004.
PA (XANT-) XANTOS BIOMEDICINE AG.
Query Match 6.7%; Score 69.5; DB 8; Length 310;
Best Local Similarity 24.2%; Pred. No. 2.6e+02;
RESULT 591
ID ABU63550 standard; protein; 351 AA.
DE Mature Mycobacterium tuberculosis 38kDa protein.
PN US6517839-B1.
PD 11-FEB-2003.
PA (RESC) UNIV CALIFORNIA.
Query Match 6.7%; Score 69.5; DB 6; Length 351;
Best Local Similarity 20.5%; Pred. No. 3.1e+02;
RESULT 592
ID AAW81359 standard; protein; 359 AA.
DE Human alpha-2-3 sialyltransferase SAT-1.
PN EP890645-A2.
PD 13-JAN-1999.
PA (SESK) SEIKAGAKU KOGYO CO LTD.
Query Match 6.7%; Score 69.5; DB 2; Length 359;
Best Local Similarity 20.9%; Pred. No. 3.2e+02;
RESULT 593
ID AAR96245 standard; protein; 373 AA.
DE Mutant subtilisin BEN' protein S86.
PN WO9609396-A1.
PD 28-MAR-1996.
PA (UYMA-) UNIV MARYLAND BALTIMORE.
Query Match 6.7%; Score 69.5; DB 2; Length 373;
Best Local Similarity 20.7%; Pred. No. 3.3e+02;
RESULT 594
ID ABB79114 standard; protein; 373 AA.
DE Mutant subtilisin BPN' protein S86 #1.
PN WO200226956-A1.
PD 04-APR-2002.
PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
Query Match 6.7%; Score 69.5; DB 5; Length 373;
Best Local Similarity 20.7%; Pred. No. 3.3e+02;
RESULT 595
ID ABB79096 standard; protein; 373 AA.
DE Mutant subtilisin BPN' protein S86.
PN WO200226956-A1.
PD 04-APR-2002.
PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
Query Match 6.7%; Score 69.5; DB 5; Length 373;
Best Local Similarity 20.7%; Pred. No. 3.3e+02;
RESULT 596
ID ABU63549 standard; protein; 373 AA.
DE Mycobacterium tuberculosis 38kDa protein.
PN US6517839-B1.
PD 13-FEB-2003.
PA (RESC) UNIV CALIFORNIA.
Query Match 6.7%; Score 69.5; DB 6; Length 373;
Best Local Similarity 20.5%; Pred. No. 3.3e+02;
RESULT 597
ID AAW64363 standard; protein; 374 AA.
DE Mycobacterium antigen Tbra3-38 kD-Tb38-1 fusion protein.
PN WO9816645-A2.
PD 23-APR-1998.
PA (CORI-) CORIXA CORP.
Query Match 6.7%; Score 69.5; DB 2; Length 374;
Best Local Similarity 20.5%; Pred. No. 3.3e+02;
RESULT 598
ID AAW64364 standard; protein; 374 AA.
DE Mycobacterium 39 kDa antigen.
PN WO9816645-A2.
PD 23-APR-1998.
PA (CORI-) CORIXA CORP.
Query Match 6.7%; Score 69.5; DB 2; Length 374;
Best Local Similarity 20.5%; Pred. No. 3.3e+02;
RESULT 599
ID AAW81730 standard; protein; 374 AA.
DE M. tuberculosis fusion protein Tbra3/38kD/Tb38-1.
PN WO9816646-A2.
PD 23-APR-1998.
PA (CORI-) CORIXA CORP.
Query Match 6.7%; Score 69.5; DB 2; Length 374;
Best Local Similarity 20.5%; Pred. No. 3.3e+02;
RESULT 600
ID AAW81731 standard; protein; 374 AA.
DE M. tuberculosis 38kD antigen protein.
PN WO9816646-A2.
PD 23-APR-1998.
PA (CORI-) CORIXA CORP.
Query Match 6.7%; Score 69.5; DB 2; Length 374;
Best Local Similarity 20.5%; Pred. No. 3.3e+02;
RESULT 601
ID AAY32061 standard; protein; 374 AA.
DE Mycobacterium tuberculosis antigen Tbra3-38kD-Tb38-1 fusion.
PN WO9951748-A2.
PD 14-OCT-1999.
PA (CORI-) CORIXA CORP.
Query Match 6.7%; Score 69.5; DB 2; Length 374;
Best Local Similarity 20.5%; Pred. No. 3.3e+02;
RESULT 602
ID AAY39018 standard; protein; 374 AA.
DE M. tuberculosis 38 kDa antigen protein.
PN WO9942118-A2.
PD 26-AUG-1999.
PA (CORI-) CORIXA CORP.
Query Match 6.7%; Score 69.5; DB 2; Length 374;
Best Local Similarity 20.5%; Pred. No. 3.3e+02;
RESULT 603
ID AAY39017 standard; protein; 374 AA.
DE M. tuberculosis fusion protein Tbra3/38kDa/Tb38-1.

PN WO9942118-A2.
PD 26-AUG-1999.
PA (CORI-) CORIXA CORP.
Query Match 6.7%; Score 69.5; DB 2; Length 374;
Best Local Similarity 20.5%; Pred. No. 3.3e+02;
RESULT 604
ID AA39161 standard; protein; 374 AA.
DE M. tuberculosis antigen 38 kD amino acid sequence.
PN WO9942076-A2.
PD 26-AUG-1999.
PA (CORI-) CORIXA CORP.
Query Match 6.7%; Score 69.5; DB 2; Length 374;
Best Local Similarity 20.5%; Pred. No. 3.3e+02;
RESULT 605
ID AA39160 standard; protein; 374 AA.
DE M. tuberculosis TbrA3, 38 kD and Tbr38-1 fusion protein.
PN WO9942076-A2.
PD 26-AUG-1999.
PA (CORI-) CORIXA CORP.
Query Match 6.7%; Score 69.5; DB 2; Length 374;
Best Local Similarity 20.5%; Pred. No. 3.3e+02;
RESULT 606
ID AA611840 standard; protein; 374 AA.
DE Mycobacterium tuberculosis 38kDa-LP protein.
PN WO200170764-A2.
PD 27-SEP-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 6.7%; Score 69.5; DB 4; Length 374;
Best Local Similarity 20.5%; Pred. No. 3.3e+02;
RESULT 607
ID AA29719 standard; protein; 374 AA.
DE Mycobacterium sp. 38kD antigenic protein.
PN WO200272792-A2.
PD 19-SEP-2002.
PA (CORI-) CORIXA CORP.
Query Match 6.7%; Score 69.5; DB 5; Length 374;
Best Local Similarity 20.5%; Pred. No. 3.3e+02;
RESULT 608
ID AA50733 standard; protein; 374 AA.
DE Mycobacterium tuberculosis immunodominant Mtb protein PhoS1 PstS1.
PN WO200204018-A2.
PD 17-JAN-2002.
PA (COLS) UNIV COLORADO STATE RES FOUND.
Query Match 6.7%; Score 69.5; DB 5; Length 374;
Best Local Similarity 20.5%; Pred. No. 3.3e+02;
RESULT 609
ID AA617583 standard; protein; 374 AA.
DE Mycobacterium species 38 kD protein.
PN WO200198460-A2.
PD 27-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match 6.7%; Score 69.5; DB 5; Length 374;
Best Local Similarity 20.5%; Pred. No. 3.3e+02;
RESULT 610
ID AAU74590 standard; protein; 374 AA.
DE Antigenic fusion protein TbrA3-38kD-Tb38-1.
PN US2002009459-A1.
PD 24-JAN-2002.
PA (REED/) REED S G.
PA (SKET/) SKIY Y A.
PA (DILL/) DILLON D C.
PA (ALDE/) ALDERSON M.
PA (CAMP/) CAMPOS-NETO A.
Query Match 6.7%; Score 69.5; DB 5; Length 374;
Best Local Similarity 20.5%; Pred. No. 3.3e+02;
RESULT 611
ID ADP69757 standard; protein; 374 AA.
DE Fusion protein #3 of M. tuberculosis antigen.
PN US2003147911-A1.
PD 07-AUG-2003.
PA (CORI-) CORIXA CORP.
Query Match 6.7%; Score 69.5; DB 7; Length 374;
Best Local Similarity 20.5%; Pred. No. 3.3e+02;

RESULT 612
ID ADP69791 standard; protein; 374 AA.
DE M. tuberculosis 38kD antigen.
PN US2003147911-A1.
PD 07-AUG-2003.
PA (CORI-) CORIXA CORP.
Query Match 6.7%; Score 69.5; DB 7; Length 374;
Best Local Similarity 20.5%; Pred. No. 3.3e+02;
RESULT 613
ID AA610702 standard; protein; 414 AA.
DE Mouse GM3 synthase (4ST3 Gal IV) protein.
PN US6280989-B1.
PD 28-AUG-2001.
PA (KAPI/) KAPITONOV D.
PA (YURK/) YU R K.
Query Match 6.7%; Score 69.5; DB 4; Length 414;
Best Local Similarity 20.9%; Pred. No. 3.8e+02;
RESULT 614
ID AAG13914 standard; protein; 443 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 13581.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.7%; Score 69.5; DB 3; Length 443;
Best Local Similarity 26.3%; Pred. No. 4.2e+02;
RESULT 615
ID AAG51514 standard; protein; 443 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65388.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.7%; Score 69.5; DB 3; Length 443;
Best Local Similarity 26.3%; Pred. No. 4.2e+02;
RESULT 616
ID AAG51513 standard; protein; 449 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65387.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.7%; Score 69.5; DB 3; Length 449;
Best Local Similarity 26.3%; Pred. No. 4.3e+02;
RESULT 617
ID AAG13913 standard; protein; 449 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 13580.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.7%; Score 69.5; DB 3; Length 449;
Best Local Similarity 26.3%; Pred. No. 4.3e+02;
RESULT 618
ID AAB95869 standard; protein; 627 AA.
DE Human protein sequence SEQ ID NO:18945.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 6.7%; Score 69.5; DB 4; Length 627;
Best Local Similarity 23.9%; Pred. No. 6.8e+02;
RESULT 619
ID AA39082 standard; protein; 652 AA.
DE M. tuberculosis fusion protein Tbp-8.
PN WO9942118-A2.
PD 26-AUG-1999.
PA (CORI-) CORIXA CORP.
Query Match 6.7%; Score 69.5; DB 2; Length 652;
Best Local Similarity 20.5%; Pred. No. 7.2e+02;
RESULT 620
ID AA39225 standard; protein; 652 AA.
DE M. tuberculosis fusion protein Tbp-8 amino acid sequence.
PN WO9942076-A2.
PD 26-AUG-1999.
PA (CORI-) CORIXA CORP.
Query Match 6.7%; Score 69.5; DB 2; Length 652;
Best Local Similarity 20.5%; Pred. No. 7.2e+02;
RESULT 621
ID ABP54926 standard; protein; 782 AA.
DE Human gelsolin.
PN WO200274982-A1.

PD 26-SEP-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 6.7%; Score 69.5; DB 5; Length 782;
Best Local Similarity 21.2%; Pred. No. 9.2e+02;
RESULT 622
ID AA64379 standard; protein; 802 AA.
DE Mycobacterium antigen TbF2 protein fusion.
PD W09816645-A2.
PD 23-APR-1998.
PA (CORI-) CORIXA CORP.
Query Match 6.7%; Score 69.5; DB 2; Length 802;
Best Local Similarity 20.5%; Pred. No. 9.5e+02;
RESULT 623
ID AA81746 standard; protein; 802 AA.
DE M. tuberculosis fusion protein TDF-2.
PD W09816646-A2.
PD 23-APR-1998.
PA (CORI-) CORIXA CORP.
Query Match 6.7%; Score 69.5; DB 2; Length 802;
Best Local Similarity 20.5%; Pred. No. 9.5e+02;
RESULT 624
ID AA32063 standard; protein; 802 AA.
DE Mycobacterium tuberculosis antigen fusion protein TbF-2.
PD W0951748-A2.
PD 14-OCT-1999.
PA (CORI-) CORIXA CORP.
Query Match 6.7%; Score 69.5; DB 2; Length 802;
Best Local Similarity 20.5%; Pred. No. 9.5e+02;
RESULT 625
ID AA39033 standard; protein; 802 AA.
DE M. tuberculosis fusion protein TbF-2.
PD W09942118-A2.
PD 26-AUG-1999.
PA (CORI-) CORIXA CORP.
Query Match 6.7%; Score 69.5; DB 2; Length 802;
Best Local Similarity 20.5%; Pred. No. 9.5e+02;
RESULT 626
ID AA39081 standard; protein; 802 AA.
DE M. tuberculosis fusion protein TbF-6.
PD W09942118-A2.
PD 26-AUG-1999.
PA (CORI-) CORIXA CORP.
Query Match 6.7%; Score 69.5; DB 2; Length 802;
Best Local Similarity 20.5%; Pred. No. 9.5e+02;
RESULT 627
ID AA39176 standard; protein; 802 AA.
DE M. tuberculosis fusion protein TbF-2 amino acid sequence.
PD W09942076-A2.
PD 26-AUG-1999.
PA (CORI-) CORIXA CORP.
Query Match 6.7%; Score 69.5; DB 2; Length 802;
Best Local Similarity 20.5%; Pred. No. 9.5e+02;
RESULT 628
ID AA39224 standard; protein; 802 AA.
DE M. tuberculosis fusion protein TbF-6 amino acid sequence.
PD W09942076-A2.
PD 26-AUG-1999.
PA (CORI-) CORIXA CORP.
Query Match 6.7%; Score 69.5; DB 2; Length 802;
Best Local Similarity 20.5%; Pred. No. 9.5e+02;
RESULT 629
ID AAU74592 standard; protein; 802 AA.
DE Antigenic fusion protein TDRa3-38KD-Tb38-1-DPEP (TbF-2).
PD US2002009459-A1.
PD 24-JAN-2002.
PA (REED/) REED S G.
PA (SKEI/) SKEIKY Y A.
PA (DILL/) DILLON D C.
PA (ALDE/) ALDERSON M.
PA (CAMP/) CAMPOS-NETO A.
Query Match 6.7%; Score 69.5; DB 5; Length 802;
Best Local Similarity 20.5%; Pred. No. 9.5e+02;
RESULT 630

ID ADF69761 standard; protein; 802 AA.
DE Fusion protein #5 of M. tuberculosis antigen.
PD US2003147911-A1.
PD 07-AUG-2003.
PA (CORI-) CORIXA CORP.
Query Match 6.7%; Score 69.5; DB 7; Length 802;
Best Local Similarity 20.5%; Pred. No. 9.5e+02;
RESULT 631
ID AEM80426 standard; protein; 899 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO80961, SEQ:1071.
PD W02004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 6.7%; Score 69.5; DB 8; Length 899;
Best Local Similarity 26.0%; Pred. No. 1.1e+03;
RESULT 632
ID AAU01901 standard; protein; 983 AA.
DE M. tuberculosis TbF15 fusion protein.
PD W0200124820-A1.
PD 12-APR-2001.
PA (CORI-) CORIXA CORP.
Query Match 6.7%; Score 69.5; DB 4; Length 983;
Best Local Similarity 20.5%; Pred. No. 1.3e+03;
RESULT 633
ID AEM85764 standard; protein; 1006 AA.
DE Mouse protein sequence mcp6001.
PD W02003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 6.7%; Score 69.5; DB 7; Length 1006;
Best Local Similarity 25.2%; Pred. No. 1.3e+03;
RESULT 634
ID AAG51511 standard; protein; 1019 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65384.
PD EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.7%; Score 69.5; DB 3; Length 1019;
Best Local Similarity 26.3%; Pred. No. 1.3e+03;
RESULT 635
ID AAG51510 standard; protein; 1025 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65383.
PD EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.7%; Score 69.5; DB 3; Length 1025;
Best Local Similarity 26.3%; Pred. No. 1.3e+03;
RESULT 636
ID ADN22624 standard; protein; 1042 AA.
DE Bacterial polypeptide #5277.
PD US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.7%; Score 69.5; DB 8; Length 1042;
Best Local Similarity 21.8%; Pred. No. 1.4e+03;
RESULT 637
ID AAU28174 standard; protein; 1053 AA.
DE Novel human secretory protein, Seq ID No 343.
PD W0200166689-A2.
PD 13-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.7%; Score 69.5; DB 4; Length 1053;
Best Local Similarity 26.0%; Pred. No. 1.4e+03;
RESULT 638
ID ADK65850 standard; protein; 1059 AA.
DE Angiogenesis-differentially expressed protein #60.
PD W02003068831-A2.
PD 14-AUG-2003.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match 6.7%; Score 69.5; DB 7; Length 1059;
Best Local Similarity 26.0%; Pred. No. 1.4e+03;

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RESULT 639
ID ADS8330 standard; protein; 1059 AA.
DE Human protein of a TNF-alpha signalling pathway protein complex Seq 185.
PN WO20004035783-A2.
PD 29-APR-2004.
PA (CELL-) CELLZOME AG.
Query Match 6.7%; Score 69.5; DB 8; Length 1059;
Best Local Similarity 26.0%; Pred. No. 1.4e+03;
RESULT 640
ID ADS61035 standard; protein; 1087 AA.
DE Human Protein Q9Y2J2, SEQ ID NO 6949.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.7%; Score 69.5; DB 7; Length 1087;
Best Local Similarity 19.8%; Pred. No. 1.4e+03;
RESULT 641
ID ADS61031 standard; protein; 1087 AA.
DE Human Protein Q9Y2J2, SEQ ID NO 6945.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.7%; Score 69.5; DB 7; Length 1087;
Best Local Similarity 19.8%; Pred. No. 1.4e+03;
RESULT 642
ID ADN72315 standard; protein; 1103 AA.
DE Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 210.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDESIGN NV.
Query Match 6.7%; Score 69.5; DB 8; Length 1103;
Best Local Similarity 20.8%; Pred. No. 1.5e+03;
RESULT 643
ID ADQ14315 standard; protein; 1424 AA.
DE Human collagen type IV alpha 3 (Goodpasture antigen).
PN WO200406262-A2.
PD 22-JUL-2004.
PA (LORA-) LORANTIS LTD.
Query Match 6.7%; Score 69.5; DB 8; Length 1424;
Best Local Similarity 48.6%; Pred. No. 2.1e+03;
RESULT 644
ID ADR41697 standard; protein; 1424 AA.
DE Human collagen (aa sequence), type IV, alpha 3 (Goodpasture antigen).
PN WO2004064863-A1.
PD 05-AUG-2004.
PA (LORA-) LORANTIS LTD.
Query Match 6.7%; Score 69.5; DB 8; Length 1424;
Best Local Similarity 48.6%; Pred. No. 2.1e+03;
RESULT 645
ID ABM84483 standard; protein; 1611 AA.
DE Human diagnostic and therapeutic pproteins Seq ID NO:4732.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.7%; Score 69.5; DB 8; Length 1611;
Best Local Similarity 48.6%; Pred. No. 2.5e+03;
RESULT 646
ID ADD47063 standard; protein; 1670 AA.
DE Human Protein NP_000082, SEQ ID NO 12751.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.7%; Score 69.5; DB 7; Length 1670;
Best Local Similarity 48.6%; Pred. No. 2.6e+03;
RESULT 647
ID ADG39875 standard; protein; 1693 AA.
DE Protein similar to human NOV16 #1.
PN US2003203843-A1.
PD 30-OCT-2003.
PA (PENA/) PENA C E A.
PA (GUOX/) GUO X.
PA (SHIM/) SHIMKETS R A.
PA (PADI/) PADIGARU M.
PA (KEKU/) KEKUDA R.
PA (SPYT/) SPYTEK K A.
PA (MEHR/) MEHRABAN F.
PA (TOPP/) TOPPER J N.
PA (MALY/) MALYANKAR U M.
PA (WASS/) WASSERMAN S M.
PA (EDIN/) EDINGER S R.
PA (SMIT/) SMITHSON G.
PA (GUNT/) GUNTHER E.
PA (KOMU/) KOMUVES L.
Query Match 6.7%; Score 69.5; DB 7; Length 1693;
Best Local Similarity 28.1%; Pred. No. 2.6e+03;
RESULT 648
ID ADM04722 standard; protein; 160 AA.
DE Human protein of the invention SEQ ID NO:3407.
PN EPI347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.7%; Score 69; DB 7; Length 160;
Best Local Similarity 37.3%; Pred. No. 1.2e+02;
RESULT 649
ID ADM67230 standard; protein; 160 AA.
DE Human homologue of murine adipocyte specific protein SeqID 600.
PN WO2004011618-A2.
PD 05-FEB-2004.
PA (HNGE-) HNGENE INC.
Query Match 6.7%; Score 69; DB 8; Length 160;
Best Local Similarity 37.3%; Pred. No. 1.2e+02;
RESULT 650
ID ABB67296 standard; protein; 181 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 28680.
PN WO2003171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.7%; Score 69; DB 4; Length 181;
Best Local Similarity 25.5%; Pred. No. 1.4e+02;
RESULT 651
ID ADD46235 standard; protein; 192 AA.
DE Human Protein Q16527, SEQ ID NO 11910.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.7%; Score 69; DB 7; Length 192;
Best Local Similarity 21.8%; Pred. No. 1.5e+02;
RESULT 652
ID ADS62637 standard; protein; 192 AA.
DE Human Protein Q16527, SEQ ID NO 8568.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.7%; Score 69; DB 7; Length 192;
Best Local Similarity 21.8%; Pred. No. 1.5e+02;
RESULT 653
ID ADS62635 standard; protein; 192 AA.
DE Rat Protein Q62908, SEQ ID NO 8566.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.7%; Score 69; DB 7; Length 192;
Best Local Similarity 21.8%; Pred. No. 1.5e+02;
RESULT 654
ID ADD46233 standard; protein; 192 AA.
DE Rat Protein Q62908, SEQ ID NO 11908.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
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Query Match	6.7%;	Score 69;	DB 7;	Length 193;
Best Local Similarity	21.8%;	Pred. No. 1.5e+02;		
RESULT 655				
ID AAW30906 standard; protein;	193 AA.			
DE Human SmlIM/CRP2 protein.				
PN WQ9733901-A1.				
PD 18-SEP-1997.				
PA (HARD) HARVARD COLLEGE.				
Query Match	6.7%;	Score 69;	DB 2;	Length 193;
Best Local Similarity	21.8%;	Pred. No. 1.5e+02;		
RESULT 656				
ID AAW30907 standard; protein;	193 AA.			
DE Mouse SmlIM/CRP2 protein.				
PN WQ9733901-A1.				
PD 18-SEP-1997.				
PA (HARD) HARVARD COLLEGE.				
Query Match	6.7%;	Score 69;	DB 2;	Length 193;
Best Local Similarity	21.8%;	Pred. No. 1.5e+02;		
RESULT 657				
ID AAB36370 standard; protein;	193 AA.			
DE Human SmlIM/CRP2 protein SEQ ID NO:1.				
PN WQ200066734-A1.				
PD 09-NOV-2000.				
PA (HARD) HARVARD COLLEGE.				
Query Match	6.7%;	Score 69;	DB 3;	Length 193;
Best Local Similarity	21.8%;	Pred. No. 1.5e+02;		
RESULT 658				
ID AAB36372 standard; protein;	193 AA.			
DE Rat SmlIM/CRP2 protein sequence SEQ ID NO:8.				
PN WQ200066734-A1.				
PD 09-NOV-2000.				
PA (HARD) HARVARD COLLEGE.				
Query Match	6.7%;	Score 69;	DB 3;	Length 193;
Best Local Similarity	21.8%;	Pred. No. 1.5e+02;		
RESULT 659				
ID AAB36377 standard; protein;	193 AA.			
DE Mouse SmlIM/CRP2 protein sequence SEQ ID NO:13.				
PN WQ200066734-A1.				
PD 09-NOV-2000.				
PA (HARD) HARVARD COLLEGE.				
Query Match	6.7%;	Score 69;	DB 3;	Length 193;
Best Local Similarity	21.8%;	Pred. No. 1.5e+02;		
RESULT 660				
ID AAE05547 standard; protein;	193 AA.			
DE Human smooth muscle cell LIM (smlIM) protein.				
PN US6259557-B1.				
PD 10-JUL-2001.				
PA (HARD) HARVARD COLLEGE.				
Query Match	6.7%;	Score 69;	DB 4;	Length 193;
Best Local Similarity	21.8%;	Pred. No. 1.5e+02;		
RESULT 661				
ID AAE05549 standard; protein;	193 AA.			
DE Rat smooth muscle cell LIM (smlIM/CRP2) protein.				
PN US6259557-B1.				
PD 10-JUL-2001.				
PA (HARD) HARVARD COLLEGE.				
Query Match	6.7%;	Score 69;	DB 4;	Length 193;
Best Local Similarity	21.8%;	Pred. No. 1.5e+02;		
RESULT 662				
ID AAE05551 standard; protein;	193 AA.			
DE Mouse smooth muscle cell LIM (smlIM/CRP2) protein.				
PN US6259557-B1.				
PD 10-JUL-2001.				
PA (HARD) HARVARD COLLEGE.				
Query Match	6.7%;	Score 69;	DB 4;	Length 193;
Best Local Similarity	21.8%;	Pred. No. 1.5e+02;		
RESULT 663				
ID ABB57213 standard; protein;	193 AA.			
DE Mouse ischaemic condition related protein sequence SEQ ID NO:22-NOV-2001.				
PN WQ200186188-A2.				
PD 22-NOV-2001.				
PA (UYNI-) UNIV NIHOH SCHOOL JURIDICAL PERSON.				
Query Match	6.7%;	Score 69;	DB 5;	Length 193;

Best Local Similarity 21.8%; Pred. No. 1.5e+02;
RESULT 664
ID ADN95293 standard; protein; 193 AA.
DE Human BEC/LEC-related protein sequence SeqID215.
FN W02003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 6.7%; Score 69; DB 7; Length 193;
Best Local Similarity 21.8%; Pred. No. 1.5e+02;
RESULT 665
ID ADQ83001 standard; protein; 193 AA.
DE Human CRP2, SEQ ID 7 & 9.
FN W02004062474-A2.
PD 29-JUL-2004.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
Query Match 6.7%; Score 69; DB 8; Length 193;
Best Local Similarity 21.8%; Pred. No. 1.5e+02;
RESULT 666
ID AAM51634 standard; protein; 203 AA.
DE Human zinc finger protein 22.
FN CN1307039-A.
PD 08-AUG-2001.
PA (BODA-) BODAO GENE TECH CO LTD SHANGHAI.
Query Match 6.7%; Score 69; DB 5; Length 203;
Best Local Similarity 22.0%; Pred. No. 1.6e+02;
RESULT 667
ID AAW14937 standard; protein; 238 AA.
DE Murine anti-porcine VCAM 3F4 light chain.
FN W09711971-A1.
PD 03-APR-1997.
PA (ALEX-) ALEXION PHARM INC.
Query Match 6.7%; Score 69; DB 2; Length 238;
Best Local Similarity 24.4%; Pred. No. 2e+02;
RESULT 668
ID AAW14942 standard; protein; 238 AA.
DE 3F4 Human IgG4 expression plasmid insert product (light chain).
FN W09711971-A1.
PD 03-APR-1997.
PA (ALEX-) ALEXION PHARM INC.
Query Match 6.7%; Score 69; DB 2; Length 238;
Best Local Similarity 24.4%; Pred. No. 2e+02;
RESULT 669
ID ADA09864 standard; protein; 247 AA.
DE Human receptor and membrane-associated protein REMAP-6, SEQ ID:6.
FN W02003070902-A2.
PD 28-AUG-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.7%; Score 69; DB 6; Length 247;
Best Local Similarity 28.2%; Pred. No. 2.1e+02;
RESULT 670
ID AAG54066 standard; protein; 308 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68898.
FN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.7%; Score 69; DB 3; Length 308;
Best Local Similarity 23.4%; Pred. No. 2.9e+02;
RESULT 671
ID AAG20021 standard; protein; 308 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 22046.
FN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.7%; Score 69; DB 3; Length 308;
Best Local Similarity 23.4%; Pred. No. 2.9e+02;
RESULT 672
ID ADC50023 standard; protein; 310 AA.
DE Gene repair function associated protein-34.1.
FN CN1382717-A.
PD 04-DEC-2002.
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
Query Match 6.7%; Score 69; DB 7; Length 310;
Best Local Similarity 25.7%; Pred. No. 2.9e+02;
RESULT 673

ID AAB94821 standard; protein; 330 AA.
DE Human protein sequence SEQ ID NO:15973.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST. 6.7%; Score 69; DB 4; Length 330;
Query Match Best Local Similarity 24.3%; Pred. No. 3.2e+02;
RESULT 674
ID AAM17010 standard; protein; 342 AA.
DE Peptide #3444 encoded by probe for measuring cervical gene expression.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match Best Local Similarity 24.5%; Pred. No. 3.3e+02;
RESULT 675
ID ABB30825 standard; peptide; 342 AA.
DE Peptide #3476 encoded by breast cell single exon nucleic acid probe.
PN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match Best Local Similarity 24.5%; Pred. No. 3.3e+02;
RESULT 676
ID ABB21410 standard; protein; 342 AA.
DE Protein #3409 encoded by probe for measuring heart cell gene expression.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match Best Local Similarity 24.5%; Pred. No. 3.3e+02;
RESULT 677
ID AAM04717 standard; protein; 342 AA.
DE Peptide #3399 encoded by probe for measuring breast gene expression.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match Best Local Similarity 24.5%; Pred. No. 3.3e+02;
RESULT 678
ID ABB38779 standard; peptide; 342 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 28444.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match Best Local Similarity 24.5%; Pred. No. 3.3e+02;
RESULT 679
ID ADB25765 standard; protein; 349 AA.
DE Human connective tissue growth factor protein encoded by SeqID 19.
PN WO2003053340-A2.
PD 03-JUL-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match Best Local Similarity 24.6%; Pred. No. 3.4e+02;
RESULT 680
ID ADB25764 standard; protein; 349 AA.
DE Human connective tissue growth factor protein encoded by SeqID 18.
PN WO2003053340-A2.
PD 03-JUL-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match Best Local Similarity 24.6%; Pred. No. 3.4e+02;
RESULT 681
ID AAM17345 standard; protein; 413 AA.
DE Peptide #3779 encoded by probe for measuring cervical gene expression.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match Best Local Similarity 22.0%; Pred. No. 4.3e+02;
RESULT 682
ID ABB36354 standard; peptide; 413 AA.

DE Peptide #3860 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match Best Local Similarity 22.0%; Pred. No. 4.3e+02;
RESULT 683
ID AAM29852 standard; protein; 413 AA.
DE Peptide #3889 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match Best Local Similarity 22.0%; Pred. No. 4.3e+02;
RESULT 684
ID ABB31159 standard; peptide; 413 AA.
DE Peptide #3810 encoded by breast cell single exon nucleic acid probe.
PN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match Best Local Similarity 22.0%; Pred. No. 4.3e+02;
RESULT 685
ID ABB21712 standard; protein; 413 AA.
DE Protein #3711 encoded by probe for measuring heart cell gene expression.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match Best Local Similarity 22.0%; Pred. No. 4.3e+02;
RESULT 686
ID AAM69513 standard; protein; 413 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 29819.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match Best Local Similarity 22.0%; Pred. No. 4.3e+02;
RESULT 687
ID AAM57121 standard; protein; 413 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 29226.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match Best Local Similarity 22.0%; Pred. No. 4.3e+02;
RESULT 688
ID ABB51187 standard; peptide; 413 AA.
DE Human liver peptide, SEQ ID NO 29835.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match Best Local Similarity 22.0%; Pred. No. 4.3e+02;
RESULT 689
ID AAM05034 standard; protein; 413 AA.
DE Peptide #3716 encoded by probe for measuring breast gene expression.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match Best Local Similarity 22.0%; Pred. No. 4.3e+02;
RESULT 690
ID ABB39138 standard; peptide; 413 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 28803.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match Best Local Similarity 22.0%; Pred. No. 4.3e+02;
RESULT 691
ID AAB94194 standard; protein; 462 AA.
DE Human protein sequence SEQ ID NO:14524.

PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST. 6.7%; Score 69; DB 4; Length 462;
Query Match 22.0%; Pred. No. 5e+02;
Best Local Similarity 22.0%; Pred. No. 5e+02;
RESULT 692
ID ABR41431 standard; protein; 474 AA.
DE Human DITHP zinc finger transcriptional regulator.
PN WO200297031-A2.
PD 05-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.7%; Score 69; DB 6; Length 474;
Best Local Similarity 24.3%; Pred. No. 5.2e+02;
RESULT 693
ID ABR85512 standard; protein; 485 AA.
DE Mouse protein sequence MCP14589.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 6.7%; Score 69; DB 7; Length 485;
Best Local Similarity 24.5%; Pred. No. 5.4e+02;
RESULT 694
ID ABR94769 standard; protein; 531 AA.
DE Human protein sequence SEQ ID NO:15851.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST. 6.7%; Score 69; DB 4; Length 531;
Query Match 29.1%; Pred. No. 6.1e+02;
Best Local Similarity 29.1%; Pred. No. 6.1e+02;
RESULT 695
ID AD067746 standard; protein; 534 AA.
DE Novel human protein sequence #2412.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.7%; Score 69; DB 8; Length 534;
Best Local Similarity 24.3%; Pred. No. 6.1e+02;
RESULT 696
ID ABR65612 standard; protein; 540 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 23628.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY. 6.7%; Score 69; DB 4; Length 540;
Query Match 42.3%; Pred. No. 6.2e+02;
Best Local Similarity 42.3%; Pred. No. 6.2e+02;
RESULT 697
ID AA79140 standard; protein; 543 AA.
DE Human haemopoietic stem cell regulatory protein SCM3.
PN WO200008145-A2.
PD 17-FEB-2000.
PA (NOVS) NOVARTIS AG.
Query Match 6.7%; Score 69; DB 3; Length 543;
Best Local Similarity 24.3%; Pred. No. 6.3e+02;
RESULT 698
ID AD809506 standard; protein; 544 AA.
DE Human protein useful for treating neurological disease Seq 3012.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.7%; Score 69; DB 8; Length 544;
Best Local Similarity 24.3%; Pred. No. 6.3e+02;
RESULT 699
ID ADQ17615 standard; protein; 553 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 432.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 6.7%; Score 69; DB 8; Length 553;
Best Local Similarity 24.3%; Pred. No. 6.4e+02;
RESULT 700
ID ADN99926 standard; protein; 558 AA.
DE Novel human protein sequence #742.

PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 6.7%; Score 69; DB 8; Length 558;
Best Local Similarity 24.3%; Pred. No. 6.5e+02;
RESULT 701
ID AAM16406 standard; protein; 605 AA.
DE Peptide #2840 encoded by probe for measuring cervical gene expression.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.7%; Score 69; DB 4; Length 605;
Best Local Similarity 21.2%; Pred. No. 7.3e+02;
RESULT 702
ID AAM18325 standard; protein; 605 AA.
DE Peptide #4759 encoded by probe for measuring cervical gene expression.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.7%; Score 69; DB 4; Length 605;
Best Local Similarity 21.2%; Pred. No. 7.3e+02;
RESULT 703
ID ABB37359 standard; peptide; 605 AA.
DE Peptide #4865 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.7%; Score 69; DB 4; Length 605;
Best Local Similarity 21.2%; Pred. No. 7.3e+02;
RESULT 704
ID ABB35394 standard; peptide; 605 AA.
DE Peptide #2900 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.7%; Score 69; DB 4; Length 605;
Best Local Similarity 21.2%; Pred. No. 7.3e+02;
RESULT 705
ID AAM28905 standard; protein; 605 AA.
DE Peptide #2942 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.7%; Score 69; DB 4; Length 605;
Best Local Similarity 21.2%; Pred. No. 7.3e+02;
RESULT 706
ID AAM30813 standard; protein; 605 AA.
DE Peptide #4850 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.7%; Score 69; DB 4; Length 605;
Best Local Similarity 21.2%; Pred. No. 7.3e+02;
RESULT 707
ID ABB30231 standard; peptide; 605 AA.
DE Peptide #2892 encoded by breast cell single exon nucleic acid probe.
PN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.7%; Score 69; DB 4; Length 605;
Best Local Similarity 21.2%; Pred. No. 7.3e+02;
RESULT 708
ID ABB32107 standard; peptide; 605 AA.
DE Peptide #4758 encoded by breast cell single exon nucleic acid probe.
PN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.7%; Score 69; DB 4; Length 605;
Best Local Similarity 21.2%; Pred. No. 7.3e+02;
RESULT 709
ID ABB20834 standard; protein; 605 AA.
DE Protein #2833 encoded by probe for measuring heart cell gene expression.
PN WO200157274-A2.

PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.7%; Score 69; DB 4; Length 605;
Best Local Similarity 21.2%; Pred. No. 7.3e+02;
RESULT 710
ID ABB22645 standard; protein; 605 AA.
DE Peptide #4644 encoded by probe for measuring heart cell gene expression.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.7%; Score 69; DB 4; Length 605;
Best Local Similarity 21.2%; Pred. No. 7.3e+02;
RESULT 711
ID AAM70489 standard; protein; 605 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 30795.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.7%; Score 69; DB 4; Length 605;
Best Local Similarity 21.2%; Pred. No. 7.3e+02;
RESULT 712
ID AAM56221 standard; protein; 605 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 28326.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.7%; Score 69; DB 4; Length 605;
Best Local Similarity 21.2%; Pred. No. 7.3e+02;
RESULT 713
ID AAM58049 standard; protein; 605 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 30154.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.7%; Score 69; DB 4; Length 605;
Best Local Similarity 21.2%; Pred. No. 7.3e+02;
RESULT 714
ID AAM04140 standard; protein; 605 AA.
DE Peptide #2822 encoded by probe for measuring breast gene expression.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.7%; Score 69; DB 4; Length 605;
Best Local Similarity 21.2%; Pred. No. 7.3e+02;
RESULT 715
ID ABG38178 standard; peptide; 605 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 27843.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.7%; Score 69; DB 5; Length 605;
Best Local Similarity 21.2%; Pred. No. 7.3e+02;
RESULT 716
ID ABG40128 standard; peptide; 605 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 29793.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.7%; Score 69; DB 5; Length 605;
Best Local Similarity 21.2%; Pred. No. 7.3e+02;
RESULT 717
ID AAM18138 standard; protein; 614 AA.
DE Peptide #4572 encoded by probe for measuring cervical gene expression.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.7%; Score 69; DB 4; Length 614;
Best Local Similarity 19.8%; Pred. No. 7.4e+02;
RESULT 718
ID ABB37171 standard; peptide; 614 AA.
DE Peptide #4677 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.7%; Score 69; DB 4; Length 614;
Best Local Similarity 19.8%; Pred. No. 7.4e+02;
RESULT 719
ID AAM30642 standard; protein; 614 AA.
DE Peptide #4679 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.7%; Score 69; DB 4; Length 614;
Best Local Similarity 19.8%; Pred. No. 7.4e+02;
RESULT 720
ID ABB31933 standard; peptide; 614 AA.
DE Peptide #4584 encoded by breast cell single exon nucleic acid probe.
PN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.7%; Score 69; DB 4; Length 614;
Best Local Similarity 19.8%; Pred. No. 7.4e+02;
RESULT 721
ID AAM57882 standard; protein; 614 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 29987.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.7%; Score 69; DB 4; Length 614;
Best Local Similarity 19.8%; Pred. No. 7.4e+02;
RESULT 722
ID AAM05768 standard; protein; 614 AA.
DE Peptide #4450 encoded by probe for measuring breast gene expression.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.7%; Score 69; DB 4; Length 614;
Best Local Similarity 19.8%; Pred. No. 7.4e+02;
RESULT 723
ID ADRI0160 standard; protein; 634 AA.
DE Human protein useful for treating neurological disease Seq 3666.
PN EPI447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.7%; Score 69; DB 8; Length 634;
Best Local Similarity 19.8%; Pred. No. 7.8e+02;
RESULT 724
ID ADN99925 standard; protein; 646 AA.
DE Novel human protein sequence #741.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 6.7%; Score 69; DB 8; Length 646;
Best Local Similarity 24.3%; Pred. No. 8e+02;
RESULT 725
ID ADC37566 standard; protein; 659 AA.
DE Human nucleic acid associated protein, NAAP-33.
PN WO2003046151-A2.
PD 05-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.7%; Score 69; DB 7; Length 659;
Best Local Similarity 21.2%; Pred. No. 8.2e+02;
RESULT 726
ID ADRI4708 standard; protein; 659 AA.
DE Human NF-kappaB pathway-associated protein SeqID780.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 6.7%; Score 69; DB 8; Length 659;
Best Local Similarity 21.2%; Pred. No. 8.2e+02;
RESULT 727
ID ADRO9687 standard; protein; 664 AA.
DE Human protein useful for treating neurological disease Seq 3193.
PN EPI447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.

Query Match 6.7%; Score 69; DB 8; Length 664;
Best Local Similarity 19.8%; Pred. No. 8.3e+02;
RESULT 728
ID ADE54856 standard; protein; 682 AA.
DE Human Protein Q02386, SEQ ID NO 661.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GENO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.7%; Score 69; DB 7; Length 682;
Best Local Similarity 24.5%; Pred. No. 8.6e+02;
RESULT 729
ID ADM96600 standard; protein; 692 AA.
DE Human integrin beta3 subunit 1JY2 (chain B) mature protein.
PN WO2004007530-A2.
PD 22-JAN-2004.
PA (BLQO) CENT BLOOD RES INC.
Query Match 6.7%; Score 69; DB 8; Length 692;
Best Local Similarity 23.2%; Pred. No. 8.8e+02;
RESULT 730
ID AAR05936 standard; protein; 718 AA.
DE Secreted GPIIb subunit of multiple subunit polypeptide (MSP) GPIIb-IIIa.
PN WO9006953-A.
PD 28-JUN-1990.
PA (GPTH) GENENTECH INC.
Query Match 6.7%; Score 69; DB 2; Length 718;
Best Local Similarity 23.2%; Pred. No. 9.2e+02;
RESULT 731
ID AAY92449 standard; protein; 762 AA.
DE GPIIa variant Asp18Tyr.
PN WO200020634-A1.
PD 13-APR-2000.
PA (NOVA-) NOVA MOLECULAR INC.
Query Match 6.7%; Score 69; DB 3; Length 762;
Best Local Similarity 23.2%; Pred. No. 1e+03;
RESULT 732
ID AAY92455 standard; protein; 762 AA.
DE GPIIa variant Arg636Cys.
PN WO200020634-A1.
PD 13-APR-2000.
PA (NOVA-) NOVA MOLECULAR INC.
Query Match 6.7%; Score 69; DB 3; Length 762;
Best Local Similarity 23.2%; Pred. No. 1e+03;
RESULT 733
ID AAY92450 standard; protein; 762 AA.
DE GPIIa variant Ser162Leu.
PN WO200020634-A1.
PD 13-APR-2000.
PA (NOVA-) NOVA MOLECULAR INC.
Query Match 6.7%; Score 69; DB 3; Length 762;
Best Local Similarity 23.2%; Pred. No. 1e+03;
RESULT 734
ID AAY92454 standard; protein; 762 AA.
DE GPIIa variant Pro407Ala.
PN WO200020634-A1.
PD 13-APR-2000.
PA (NOVA-) NOVA MOLECULAR INC.
Query Match 6.7%; Score 69; DB 3; Length 762;
Best Local Similarity 23.2%; Pred. No. 1e+03;
RESULT 735
ID AAY92451 standard; protein; 762 AA.
DE GPIIa variant Arg214Gln.
PN WO200020634-A1.
PD 13-APR-2000.
PA (NOVA-) NOVA MOLECULAR INC.
Query Match 6.7%; Score 69; DB 3; Length 762;
Best Local Similarity 23.2%; Pred. No. 1e+03;
RESULT 736
ID AAY92456 standard; protein; 762 AA.
DE GPIIa variant Ser752Pro.
PN WO200020634-A1.
PD 13-APR-2000.
PA (NOVA-) NOVA MOLECULAR INC.
Query Match 6.7%; Score 69; DB 3; Length 762;
Best Local Similarity 23.2%; Pred. No. 1e+03;
RESULT 737
ID AAY92452 standard; protein; 762 AA.
DE GPIIa variant Arg214Trp.
PN WO200020634-A1.
PD 13-APR-2000.
PA (NOVA-) NOVA MOLECULAR INC.
Query Match 6.7%; Score 69; DB 3; Length 762;
Best Local Similarity 23.2%; Pred. No. 1e+03;
RESULT 738
ID AAY92448 standard; protein; 762 AA.
DE GPIIa variant Leu17Trp.
PN WO200020634-A1.
PD 13-APR-2000.
PA (NOVA-) NOVA MOLECULAR INC.
Query Match 6.7%; Score 69; DB 3; Length 762;
Best Local Similarity 23.2%; Pred. No. 1e+03;
RESULT 739
ID ADN99955 standard; protein; 776 AA.
DE Novel human protein sequence #771.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 6.7%; Score 69; DB 8; Length 776;
Best Local Similarity 24.5%; Pred. No. 1e+03;
RESULT 740
ID AAR51500 standard; protein; 788 AA.
DE Human platelet GPIIa surface antigen Yuk-a.
PN JP06078771-A.
PD 22-MAR-1994.
PA (JUJI/) JUJI T.
Query Match 6.7%; Score 69; DB 2; Length 788;
Best Local Similarity 23.2%; Pred. No. 1e+03;
RESULT 741
ID AAY49567 standard; protein; 788 AA.
DE Human antithrombin III protein sequence.
PN WO9950454-A2.
PD 07-OCT-1999.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
Query Match 6.7%; Score 69; DB 2; Length 788;
Best Local Similarity 23.2%; Pred. No. 1e+03;
RESULT 742
ID AAY49553 standard; protein; 788 AA.
DE Human endothelial membrane glycoprotein IIIa protein sequence.
PN WO9950454-A2.
PD 07-OCT-1999.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
Query Match 6.7%; Score 69; DB 3; Length 788;
Best Local Similarity 23.2%; Pred. No. 1e+03;
RESULT 743
ID AAY81461 standard; protein; 788 AA.
DE Human integrin beta 3.
PN US6037176-A.
PD 14-MAR-2000.
PA (ISIS-) ISIS PHARM INC.
Query Match 6.7%; Score 69; DB 3; Length 788;
Best Local Similarity 23.2%; Pred. No. 1e+03;
RESULT 744
ID AAY92444 standard; protein; 788 AA.
DE Variant human GPIIa, alloantigen PIA2.
PN WO200020634-A1.
PD 13-APR-2000.
PA (NOVA-) NOVA MOLECULAR INC.
Query Match 6.7%; Score 69; DB 3; Length 788;
Best Local Similarity 23.2%; Pred. No. 1e+03;
RESULT 745
ID AAY92443 standard; protein; 788 AA.
DE Wild type human GPIIa, alloantigen PIA1.
PN WO200020634-A1.
PD 13-APR-2000.
PA (NOVA-) NOVA MOLECULAR INC.
Query Match 6.7%; Score 69; DB 3; Length 788;

Best Local Similarity 23.2%; Pred. No. 1e+03;
RESULT 746
ID AAU76336 standard; peptide; 788 AA.
DE Human anti-dual integrin protein #2.
PN WO200212501-A2.
PD 14-FEB-2002.
PA (CENZ) CENTOCOR INC.
Query Match 6.7%; Score 69; DB 5; Length 788;
Best Local Similarity 23.2%; Pred. No. 1e+03;
RESULT 747
ID AAE21036 standard; protein; 788 AA.
DE Human beta 3 protein.
PN WO200208280-A2.
PD 31-JAN-2002.
PA (BURN-) BURNHAM INST.
Query Match 6.7%; Score 69; DB 5; Length 788;
Best Local Similarity 23.2%; Pred. No. 1e+03;
RESULT 748
ID AAE21038 standard; protein; 788 AA.
DE Human beta 3 mutant protein (N69T, L70Q).
PN WO200208280-A2.
PD 31-JAN-2002.
PA (BURN-) BURNHAM INST.
Query Match 6.7%; Score 69; DB 5; Length 788;
Best Local Similarity 23.2%; Pred. No. 1e+03;
RESULT 749
ID ABG74668 standard; protein; 788 AA.
DE Human ITGB3 protein.
PN WO2003016494-A2.
PD 27-FEB-2003.
PA (VITI-) VITIVITY INC.
Query Match 6.7%; Score 69; DB 6; Length 788;
Best Local Similarity 23.2%; Pred. No. 1e+03;
RESULT 750
ID AAO27099 standard; protein; 788 AA.
DE Human integrin beta-3 precursor (CD61).
PN WO2003010130-A2.
PD 06-FEB-2003.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
PA (BIOA-) BIOACTA LTD.
Query Match 6.7%; Score 69; DB 6; Length 788;
Best Local Similarity 23.2%; Pred. No. 1e+03;
RESULT 751
ID ABB82768 standard; protein; 788 AA.
DE Human alphaVbeta3 integrin beta3 subunit sequence.
PN WO200287505-A2.
PD 07-NOV-2002.
PA (GEO) GEN HOSPITAL CORP.
Query Match 6.7%; Score 69; DB 6; Length 788;
Best Local Similarity 23.2%; Pred. No. 1e+03;
RESULT 752
ID ADA21006 standard; protein; 788 AA.
DE Human beta 3 polypeptide.
PN US2003064471-A1.
PD 03-APR-2003.
PA (SHEP/) SHEPPARD D.
PA (PYTE/) PYTELA R.
Query Match 6.7%; Score 69; DB 7; Length 788;
Best Local Similarity 23.2%; Pred. No. 1e+03;
RESULT 753
ID ADM99599 standard; protein; 788 AA.
DE Human integrin beta3 subunit precursor protein.
PN WO2004007530-A2.
PD 22-JAN-2004.
PA (BLOO-) CENT BLOOD RES INC.
Query Match 6.7%; Score 69; DB 8; Length 788;
Best Local Similarity 23.2%; Pred. No. 1e+03;
RESULT 754
ID ADN88935 standard; protein; 788 AA.
DE Human integrin beta 3 protein for generating hyperlipidemia treatment.
PN WO2004033710-A2.
PD 22-APR-2004.

PA (GENA-) GENAISSANCE PHARM INC.
Query Match 6.7%; Score 69; DB 8; Length 788;
Best Local Similarity 23.2%; Pred. No. 1e+03;
RESULT 755
ID ADQ14323 standard; protein; 788 AA.
DE Human platelet glycoprotein IIIa (GPIIIa).
PN WO2004060262-A2.
PD 22-JUL-2004.
PA (LORA-) LORANTIS LTD.
Query Match 6.7%; Score 69; DB 8; Length 788;
Best Local Similarity 23.2%; Pred. No. 1e+03;
RESULT 756
ID ADR41704 standard; protein; 788 AA.
DE Human platelet glycoprotein IIIa (GPIIIa).
PN WO2004064863-A1.
PD 05-AUG-2004.
PA (LORA-) LORANTIS LTD.
Query Match 6.7%; Score 69; DB 8; Length 788;
Best Local Similarity 23.2%; Pred. No. 1e+03;
RESULT 757
ID ADP23744 standard; protein; 788 AA.
DE PRO polypeptide SEQ ID NO:922.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 6.7%; Score 69; DB 8; Length 788;
Best Local Similarity 23.2%; Pred. No. 1e+03;
RESULT 758
ID ADP23742 standard; protein; 794 AA.
DE PRO polypeptide SEQ ID NO:920.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 6.7%; Score 69; DB 8; Length 794;
Best Local Similarity 23.2%; Pred. No. 1.1e+03;
RESULT 759
ID ADR08812 standard; protein; 882 AA.
DE Human protein useful for treating neurological disease Seq 2318.
PN EPI447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.7%; Score 69; DB 8; Length 882;
Best Local Similarity 25.7%; Pred. No. 1.2e+03;
RESULT 760
ID ADE08747 standard; protein; 901 AA.
DE Novel protein (useful for identifying genetic disorders) #902.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 6.7%; Score 69; DB 7; Length 901;
Best Local Similarity 25.0%; Pred. No. 1.3e+03;
RESULT 761
ID AAM25587 standard; protein; 945 AA.
DE Human protein sequence SEQ ID NO:1102.
PN WO200153455-A2.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.7%; Score 69; DB 4; Length 945;
Best Local Similarity 22.6%; Pred. No. 1.3e+03;
RESULT 762
ID ABB65540 standard; protein; 1013 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 23412.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.7%; Score 69; DB 4; Length 1013;
Best Local Similarity 24.7%; Pred. No. 1.5e+03;
RESULT 763
ID ABB60992 standard; protein; 1186 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 9768.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 6.7%; Score 69; DB 4; Length 1186;
Best Local Similarity 23.5%; Pred. No. 1.8e+03;
RESULT 764
ID ADQ89666 standard; protein; 2228 AA.
DE Antagonist of cell cycle progression polypeptide #48.
PN WO2004063362-A2.
PD 29-JUL-2004.
PA (CYCL-) CYCLACEL LTD.
Query Match 6.7%; Score 69; DB 8; Length 2228;
Best Local Similarity 19.4%; Pred. No. 4.3e+03;
RESULT 765
ID AAB79246 standard; protein; 114 AA.
DE Corynebacterium glutamicum SMP protein sequence SEQ ID NO:8.
PN WO200100844-A2.
PD 04-JAN-2001.
PA (BADI) BASF AG.
Query Match 6.6%; Score 68.5; DB 4; Length 114;
Best Local Similarity 33.3%; Pred. No. 83;
RESULT 766
ID ADH87605 standard; protein; 138 AA.
DE Enterococcus faecalis polypeptide #2085.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 6.6%; Score 68.5; DB 7; Length 138;
Best Local Similarity 22.2%; Pred. No. 1.1e+02;
RESULT 767
ID AAG92407 standard; protein; 157 AA.
DE C glutamicum protein fragment SEQ ID NO: 6161.
PN EP108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 6.6%; Score 68.5; DB 4; Length 157;
Best Local Similarity 33.3%; Pred. No. 1.3e+02;
RESULT 768
ID ABB08759 standard; protein; 157 AA.
DE Corynebacterium glutamicum rpi SEQ ID NO 2.
PN DE10037612-A1.
PD 14-FEB-2002.
PA (DEGS) DEGUSSA AG.
Query Match 6.6%; Score 68.5; DB 5; Length 157;
Best Local Similarity 33.3%; Pred. No. 1.3e+02;
RESULT 769
ID ADR09469 standard; protein; 161 AA.
DE Human protein useful for treating neurological disease Seq 2975.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.6%; Score 68.5; DB 8; Length 161;
Best Local Similarity 24.2%; Pred. No. 1.3e+02;
RESULT 770
ID AAG42639 standard; protein; 276 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 53199.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.6%; Score 68.5; DB 3; Length 276;
Best Local Similarity 20.8%; Pred. No. 2.8e+02;
RESULT 771
ID ADOS8683 standard; protein; 338 AA.
DE Human regulatory molecule HRM-4.
PN US2002058264-A1.
PD 16-MAY-2002.
PA (INCY-) INCYTE PHARM INC.
Query Match 6.6%; Score 68.5; DB 8; Length 338;
Best Local Similarity 19.0%; Pred. No. 3.7e+02;
RESULT 772
ID ABUI1001 standard; protein; 372 AA.
DE cDNA encoding human cancer promoting protein SP2114b.
PN CN1351082-A.
PD 29-MAY-2002.
PA (SHAN-) SHANGHAI INST ONCOLOGY.
Query Match 6.6%; Score 68.5; DB 5; Length 372;

Best Local Similarity 19.0%; Pred. No. 4.2e+02;
RESULT 773
ID ABB79110 standard; protein; 373 AA.
DE Mutant subtilisin BPN' protein S3C Q206C.
PN WO200226956-A1.
PD 04-APR-2002.
PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
Query Match 6.6%; Score 68.5; DB 5; Length 373;
Best Local Similarity 20.3%; Pred. No. 4.2e+02;
RESULT 774
ID ABB79100 standard; protein; 373 AA.
DE Mutant subtilisin BPN' protein #2.
PN WO200226956-A1.
PD 04-APR-2002.
PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
Query Match 6.6%; Score 68.5; DB 5; Length 373;
Best Local Similarity 20.3%; Pred. No. 4.2e+02;
RESULT 775
ID AAR30090 standard; protein; 374 AA.
DE 38 kDa lipoprotein antigen.
PN WO9221697-A2.
PD 10-DEC-1992.
PA (MEDI-) MEDICAL RES COUNCIL.
Query Match 6.6%; Score 68.5; DB 2; Length 374;
Best Local Similarity 21.1%; Pred. No. 4.2e+02;
RESULT 776
ID AAM41337 standard; protein; 403 AA.
DE Human polypeptide SEQ ID NO 6268.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.6%; Score 68.5; DB 4; Length 403;
Best Local Similarity 19.0%; Pred. No. 4.7e+02;
RESULT 777
ID AAM39551 standard; protein; 412 AA.
DE Human polypeptide SEQ ID NO 2696.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.6%; Score 68.5; DB 4; Length 412;
Best Local Similarity 19.0%; Pred. No. 4.8e+02;
RESULT 778
ID ADS44221 standard; protein; 528 AA.
DE Bacterial polypeptide #22651.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.6%; Score 68.5; DB 8; Length 528;
Best Local Similarity 22.7%; Pred. No. 6.8e+02;
RESULT 779
ID AAY86212 standard; protein; 548 AA.
DE Nuclear transport protein clone hfb101-1 protein sequence.
PN WO9964455-A1.
PD 16-DEC-1999.
PA (HELI-) HELIX RES INST.
Query Match 6.6%; Score 68.5; DB 3; Length 548;
Best Local Similarity 19.0%; Pred. No. 7.2e+02;
RESULT 780
ID ABB62204 standard; protein; 556 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 13404.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.6%; Score 68.5; DB 4; Length 556;
Best Local Similarity 26.9%; Pred. No. 7.3e+02;
RESULT 781
ID AAM40771 standard; protein; 561 AA.
DE Human polypeptide SEQ ID NO 5702.
PN WO200153312-A1.

PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC. 6.6%; Score 68.5; DB 4; Length 561;
Query Match 24.2%; Pred. No. 7.4e+02;
Best Local Similarity 23.4%; Pred. No. 1.2e+03;
RESULT 782
ID AAY86213 standard; protein; 621 AA.
DE Nuclear transport protein clone htb101-2 protein sequence.
PN WO9964455-A1.
PD 16-DEC-1999.
PA (HELI-) HELIX RES INST. 6.6%; Score 68.5; DB 3; Length 621;
Query Match 19.0%; Pred. No. 8.5e+02;
Best Local Similarity 19.0%; Pred. No. 8.5e+02;
RESULT 783
ID ABR59715 standard; protein; 621 AA.
DE Human zinc finger protein 274.
PN WO2003029277-A2.
PD 10-APR-2003.
PA (RIGE-) RIGEL PHARM INC. 6.6%; Score 68.5; DB 6; Length 621;
Query Match 19.0%; Pred. No. 8.5e+02;
Best Local Similarity 19.0%; Pred. No. 8.5e+02;
RESULT 784
ID ABB78784 standard; protein; 653 AA.
DE Human DNA repair protein 71.83 SEQ ID NO:2.
PN CN1331206-A.
PD 16-JAN-2002.
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
Query Match 6.6%; Score 68.5; DB 5; Length 653;
Best Local Similarity 19.0%; Pred. No. 9.1e+02;
RESULT 785
ID ABG73501 standard; protein; 653 AA.
DE Human SP2114a protein SEQ ID NO 20.
PN CN1351079-A.
PD 29-MAY-2002.
PA (SHAN-) SHANGHAI INST ONCOLOGY.
Query Match 6.6%; Score 68.5; DB 5; Length 653;
Best Local Similarity 19.0%; Pred. No. 9.1e+02;
RESULT 786
ID ADO00972 standard; protein; 660 AA.
DE Human homologue of Fruit fly AD-related protein CG5009.
PN US2004067535-A1.
PD 08-APR-2004.
PA (LIFE-) LIFE SCI DEV CORP. 6.6%; Score 68.5; DB 8; Length 660;
Query Match 23.7%; Pred. No. 9.2e+02;
Best Local Similarity 23.7%; Pred. No. 9.2e+02;
RESULT 787
ID ADP24645 standard; protein; 660 AA.
DE PRO polypeptide SEQ ID NO:1823.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH-) GENENTECH INC. 6.6%; Score 68.5; DB 8; Length 660;
Query Match 23.7%; Pred. No. 9.2e+02;
Best Local Similarity 23.7%; Pred. No. 9.2e+02;
RESULT 788
ID ADR08749 standard; protein; 687 AA.
DE Human protein useful for treating neurological disease Seq 2255.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY. 6.6%; Score 68.5; DB 8; Length 687;
Query Match 25.3%; Pred. No. 9.8e+02;
Best Local Similarity 25.3%; Pred. No. 9.8e+02;
RESULT 789
ID ADP74160 standard; protein; 783 AA.
DE Human novel brain/hippocampus protein #48.
PN JP2003009886-A.
PD 14-JAN-2003.
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
Query Match 6.6%; Score 68.5; DB 7; Length 783;
Best Local Similarity 23.4%; Pred. No. 1.2e+03;
RESULT 790
ID AAE37030 standard; protein; 807 AA.
DE Human nucleic acid associated protein (NAAP)-17.
PN WO2003006618-A2.

PD 23-JAN-2003.
PA (INCY-) INCYTE GENOMICS INC. 6.6%; Score 68.5; DB 6; Length 807;
Query Match 23.4%; Pred. No. 1.2e+03;
Best Local Similarity 23.4%; Pred. No. 1.2e+03;
RESULT 791
ID AAB53128 standard; protein; 829 AA.
DE Macaca mulatta rhadinovirus 17577 RRV ORF8 protein SEQ ID NO:13.
PN WO20028040-A2.
PD 18-MAY-2000.
PA (UVOR-) UNIV OREGON HEALTH SCI. 6.6%; Score 68.5; DB 3; Length 829;
Query Match 27.7%; Pred. No. 1.3e+03;
Best Local Similarity 27.7%; Pred. No. 1.3e+03;
RESULT 792
ID ADI27628 standard; protein; 914 AA.
DE Human SCUBE3-1 protein.
PN US2003219813-A1.
PD 27-NOV-2003.
PA (MILL-) MILLENNIUM PHARM INC. 6.6%; Score 68.5; DB 8; Length 914;
Query Match 21.1%; Pred. No. 1.4e+03;
Best Local Similarity 21.1%; Pred. No. 1.4e+03;
RESULT 793
ID ABB70304 standard; protein; 984 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 37704.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY. 6.6%; Score 68.5; DB 4; Length 984;
Query Match 24.5%; Pred. No. 1.6e+03;
Best Local Similarity 24.5%; Pred. No. 1.6e+03;
RESULT 794
ID ABB71862 standard; protein; 1309 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 42378.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY. 6.6%; Score 68.5; DB 4; Length 1309;
Query Match 27.0%; Pred. No. 2.4e+03;
Best Local Similarity 27.0%; Pred. No. 2.4e+03;
RESULT 795
ID ABG07111 standard; protein; 1456 AA.
DE Novel human diagnostic protein #7102.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC. 6.6%; Score 68.5; DB 4; Length 1456;
Query Match 21.8%; Pred. No. 2.7e+03;
Best Local Similarity 21.8%; Pred. No. 2.7e+03;
RESULT 796
ID ABG24514 standard; protein; 1456 AA.
DE Novel human diagnostic protein #24505.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC. 6.6%; Score 68.5; DB 4; Length 1456;
Query Match 21.8%; Pred. No. 2.7e+03;
Best Local Similarity 21.8%; Pred. No. 2.7e+03;
RESULT 797
ID ADK71824 standard; protein; 1638 AA.
DE Human kinase and phosphatase KPP-1 protein.
PN WO2004018641-A2.
PD 04-MAR-2004.
PA (INCY-) INCYTE CORP. 6.6%; Score 68.5; DB 8; Length 1638;
Query Match 26.2%; Pred. No. 3.2e+03;
Best Local Similarity 26.2%; Pred. No. 3.2e+03;
RESULT 798
ID ADE47740 standard; protein; 1664 AA.
DE Human NOV32b protein SEQ ID NO:102.
PN WO2003076642-A2.
PD 18-SEP-2003.
PA (CURA-) CURAGEN CORP. 6.6%; Score 68.5; DB 7; Length 1664;
Query Match 26.2%; Pred. No. 3.3e+03;
Best Local Similarity 26.2%; Pred. No. 3.3e+03;
RESULT 799
ID ADJ79010 standard; protein; 1664 AA.
DE Human NOVX protein Nov32B amino acid sequence.
PN US2004014053-A1.
PD 22-JAN-2004.

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PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (KEKU/) KEKUDA R.
PA (MILL/) MILLER C E.
PA (RIEG/) RIEGER D K.
PA (PENA/) PENA C E A.
PA (SHIM/) SHIMKETS R A.
PA (LILL/) LI L.
PA (BERG/) BERGHS C.
PA (ZHON/) ZHONG M.
PA (CASM/) CASMAN S J.
PA (VOSS/) VOSS E Z.
PA (BOLD/) BOLDOG F L.
PA (PADI/) PADIGARU M.
PA (SMIT/) SMITHSON G.
PA (JIWW/) JI W.
PA (GORM/) GORMAN L.
PA (VERN/) VERNET C A M.
PA (LEIT/) LEITE M W.
PA (GUOX/) GUO X S.
PA (ANDE/) ANDERSON D W.
PA (SPYT/) SPYTEK K A.
PA (GERL/) GERLACH V.
PA (BURG/) BURGESS C E.
PA (KHRA/) KHRAMTSOV N V.
PA (ORTT/) ORT T.
PA (ELLE/) ELLERMAN K.
PA (RASI/) RASTELLI L.
PA (AGEE/) AGEE M L.
PA (CHAU/) CHAUDHURI A.
PA (CHAN/) CHANT J S.
PA (DIPI/) DIPIPPO V A.
PA (EDIN/) EDINGER S R.
PA (EISE/) EISEN A J.
PA (GANG/) GANGOLLI E A.
PA (GIOT/) GIOT L.
PA (OOIC/) OOI C E.
PA (ROTH/) ROTHENBERG M E.
PA (SPAD/) SPADERNA S K.
PA (HJAL/) HJALT T.
PA (LIUX/) LIU X.
PA (TAUP/) TAUPIER R J.
PA (CATT/) CATTERTON E.
PA (SHEN/) SHENOY S G.
Query Match
Best Local Similarity 6.6%; Score 68.5; DB 8; Length 1664;
RESULT 800
ID AAE21707 standard; protein; 1719 AA.
DE Human PKIN-2 protein.
PN WO200218557-A2.
PD 07-MAR-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 6.6%; Score 68.5; DB 5; Length 1719;
RESULT 801
ID ADF89991 standard; protein; 1732 AA.
DE Human serine/threonine kinase polypeptide.
PN WO2003097822-A1.
PD 27-NOV-2003.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 6.6%; Score 68.5; DB 8; Length 1732;
RESULT 802
ID ADS93536 standard; protein; 1732 AA.
DE Human WRCK2 protein sequence SeqID2.
PN WO2004033638-A2.
PD 22-APR-2004.
PA (AMHP) WYETH.
PA (LIUW/) LIU W.
PA (WULL/) WU L.
Query Match
Best Local Similarity 6.6%; Score 68.5; DB 8; Length 1732;
RESULT 803
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (KEKU/) KEKUDA R.
PA (MILL/) MILLER C E.
PA (RIEG/) RIEGER D K.
PA (PENA/) PENA C E A.
PA (SHIM/) SHIMKETS R A.
PA (LILL/) LI L.
PA (BERG/) BERGHS C.
PA (ZHON/) ZHONG M.
PA (CASM/) CASMAN S J.
PA (VOSS/) VOSS E Z.
PA (BOLD/) BOLDOG F L.
PA (PADI/) PADIGARU M.
PA (SMIT/) SMITHSON G.
PA (JIWW/) JI W.
PA (GORM/) GORMAN L.
PA (VERN/) VERNET C A M.
PA (LEIT/) LEITE M W.
PA (GUOX/) GUO X S.
PA (ANDE/) ANDERSON D W.
PA (SPYT/) SPYTEK K A.
PA (GERL/) GERLACH V.
PA (BURG/) BURGESS C E.
PA (KHRA/) KHRAMTSOV N V.
PA (ORTT/) ORT T.
PA (ELLE/) ELLERMAN K.
PA (RASI/) RASTELLI L.
PA (AGEE/) AGEE M L.
PA (CHAU/) CHAUDHURI A.
PA (CHAN/) CHANT J S.
PA (DIPI/) DIPIPPO V A.
PA (EDIN/) EDINGER S R.
PA (EISE/) EISEN A J.
PA (GANG/) GANGOLLI E A.
PA (GIOT/) GIOT L.
PA (OOIC/) OOI C E.
PA (ROTH/) ROTHENBERG M E.
PA (SPAD/) SPADERNA S K.
PA (HJAL/) HJALT T.
PA (LIUX/) LIU X.
PA (TAUP/) TAUPIER R J.
PA (CATT/) CATTERTON E.
PA (SHEN/) SHENOY S G.
Query Match
Best Local Similarity 6.6%; Score 68.5; DB 8; Length 1738;
RESULT 804
ID ADJ79008 standard; protein; 1738 AA.
DE Human NOVX protein Nov32A amino acid sequence.
PN US2004014053-A1.
PD 22-JAN-2004.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (KEKU/) KEKUDA R.
PA (MILL/) MILLER C E.
PA (RIEG/) RIEGER D K.
PA (PENA/) PENA C E A.
PA (SHIM/) SHIMKETS R A.
PA (LILL/) LI L.
PA (BERG/) BERGHS C.
PA (ZHON/) ZHONG M.
PA (CASM/) CASMAN S J.
PA (VOSS/) VOSS E Z.
PA (BOLD/) BOLDOG F L.
PA (PADI/) PADIGARU M.
PA (SMIT/) SMITHSON G.
PA (JIWW/) JI W.
PA (GORM/) GORMAN L.
PA (VERN/) VERNET C A M.
PA (LEIT/) LEITE M W.
PA (GUOX/) GUO X S.
PA (ANDE/) ANDERSON D W.
PA (SPYT/) SPYTEK K A.
PA (GERL/) GERLACH V.
PA (BURG/) BURGESS C E.
PA (KHRA/) KHRAMTSOV N V.
PA (ORTT/) ORT T.
PA (ELLE/) ELLERMAN K.
PA (RASI/) RASTELLI L.
PA (AGEE/) AGEE M L.
PA (CHAU/) CHAUDHURI A.
PA (CHAN/) CHANT J S.
PA (DIPI/) DIPIPPO V A.
PA (EDIN/) EDINGER S R.
PA (EISE/) EISEN A J.
PA (GANG/) GANGOLLI E A.
PA (GIOT/) GIOT L.
PA (OOIC/) OOI C E.
PA (ROTH/) ROTHENBERG M E.
PA (SPAD/) SPADERNA S K.
PA (HJAL/) HJALT T.
PA (LIUX/) LIU X.
PA (TAUP/) TAUPIER R J.
PA (CATT/) CATTERTON E.
PA (SHEN/) SHENOY S G.
Query Match
Best Local Similarity 6.6%; Score 68.5; DB 8; Length 1738;
RESULT 805
ID AAE25099 standard; protein; 1770 AA.
DE Human kinase and phosphatase-19 (KAP-19) protein.
PN WO200246384-A2.
PD 13-JUN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 6.6%; Score 68.5; DB 5; Length 1770;
RESULT 806
ID ADO67825 standard; protein; 191 AA.
DE Novel human protein sequence #2491.
PN EPI440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 6.6%; Score 68; DB 8; Length 191;

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Best Local Similarity 20.5%; Pred. No. 1.9e+02;
RESULT 807
ID AAB86357 standard; protein; 194 AA.
DE Human MLP protein.
PN WO200157208-A2.
PD 09-AUG-2001.
PA (SCHD ) SCHERING AG.
Query Match 6.6%; Score 68; DB 4; Length 194;
Best Local Similarity 20.4%; Pred. No. 1.9e+02;
RESULT 808
ID AAU28055 standard; protein; 194 AA.
DE Novel human secretory protein, Seq ID No 224.
PN WO200166689-A2.
PD 13-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.6%; Score 68; DB 4; Length 194;
Best Local Similarity 20.4%; Pred. No. 1.9e+02;
RESULT 809
ID ABU06490 standard; protein; 211 AA.
DE Maize SSI glycosyl transferase domain (GLYTR) related protein #9.
PN WO200279410-A2.
PD 10-OCT-2002.
PA (BADI ) BASF PLANT SCI GMBH.
Query Match 6.6%; Score 68; DB 6; Length 211;
Best Local Similarity 24.6%; Pred. No. 2.2e+02;
RESULT 810
ID ABU06487 standard; protein; 211 AA.
DE Maize SSI glycosyl transferase domain (GLYTR) related protein #6.
PN WO200279410-A2.
PD 10-OCT-2002.
PA (BADI ) BASF PLANT SCI GMBH.
Query Match 6.6%; Score 68; DB 6; Length 211;
Best Local Similarity 24.6%; Pred. No. 2.2e+02;
RESULT 811
ID ABU06488 standard; protein; 211 AA.
DE Maize SSI glycosyl transferase domain (GLYTR) related protein #7.
PN WO200279410-A2.
PD 10-OCT-2002.
PA (BADI ) BASF PLANT SCI GMBH.
Query Match 6.6%; Score 68; DB 6; Length 211;
Best Local Similarity 24.6%; Pred. No. 2.2e+02;
RESULT 812
ID ABU06489 standard; protein; 211 AA.
DE Maize SSI glycosyl transferase domain (GLYTR) related protein #8.
PN WO200279410-A2.
PD 10-OCT-2002.
PA (BADI ) BASF PLANT SCI GMBH.
Query Match 6.6%; Score 68; DB 6; Length 211;
Best Local Similarity 24.6%; Pred. No. 2.2e+02;
RESULT 813
ID ABU06492 standard; protein; 211 AA.
DE Maize SSI glycosyl transferase domain (GLYTR) related protein #11.
PN WO200279410-A2.
PD 10-OCT-2002.
PA (BADI ) BASF PLANT SCI GMBH.
Query Match 6.6%; Score 68; DB 6; Length 211;
Best Local Similarity 24.6%; Pred. No. 2.2e+02;
RESULT 814
ID AAU16498 standard; protein; 216 AA.
DE Human novel secreted protein, Seq ID 1451.
PN WO200155322-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.6%; Score 68; DB 4; Length 216;
Best Local Similarity 22.6%; Pred. No. 2.3e+02;
RESULT 815
ID ASU55567 standard; protein; 216 AA.
DE Human novel polypeptide #654.
PN US2002132753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.

Query Match 6.6%; Score 68; DB 6; Length 216;
Best Local Similarity 22.6%; Pred. No. 2.3e+02;
RESULT 816
ID ABC28090 standard; protein; 223 AA.
DE Novel human diagnostic protein #28081.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.6%; Score 68; DB 4; Length 223;
Best Local Similarity 21.0%; Pred. No. 2.4e+02;
RESULT 817
ID AAW71876 standard; protein; 239 AA.
DE Anti-human Fas humanised antibody CH11 light chain VL-KY.
PN EP866131-A2.
PD 23-SEP-1998.
PA (SANY ) SANKYO CO LTD.
Query Match 6.6%; Score 68; DB 2; Length 239;
Best Local Similarity 24.4%; Pred. No. 2.6e+02;
RESULT 818
ID AAW71879 standard; protein; 239 AA.
DE Anti-human Fas humanised antibody CH11 light chain VL-RF.
PN EP866131-A2.
PD 23-SEP-1998.
PA (SANY ) SANKYO CO LTD.
Query Match 6.6%; Score 68; DB 2; Length 239;
Best Local Similarity 24.4%; Pred. No. 2.6e+02;
RESULT 819
ID AAW71878 standard; protein; 239 AA.
DE Anti-human Fas humanised antibody CH11 light chain VL-RY.
PN EP866131-A2.
PD 23-SEP-1998.
PA (SANY ) SANKYO CO LTD.
Query Match 6.6%; Score 68; DB 2; Length 239;
Best Local Similarity 24.4%; Pred. No. 2.6e+02;
RESULT 820
ID AAW71877 standard; protein; 239 AA.
DE Anti-human Fas humanised antibody CH11 light chain VL-KF.
PN EP866131-A2.
PD 23-SEP-1998.
PA (SANY ) SANKYO CO LTD.
Query Match 6.6%; Score 68; DB 2; Length 239;
Best Local Similarity 24.4%; Pred. No. 2.6e+02;
RESULT 821
ID AAB12914 standard; protein; 239 AA.
DE Anti-human Fas immunoglobulin M light chain protein sequence SEQ ID #80.
PN JP2000154149-A.
PD 06-JUN-2000.
PA (SANY ) SANKYO CO LTD.
Query Match 6.6%; Score 68; DB 3; Length 239;
Best Local Similarity 24.4%; Pred. No. 2.6e+02;
RESULT 822
ID AAB12916 standard; protein; 239 AA.
DE Anti-human Fas immunoglobulin M light chain protein sequence SEQ ID #84.
PN JP2000154149-A.
PD 06-JUN-2000.
PA (SANY ) SANKYO CO LTD.
Query Match 6.6%; Score 68; DB 3; Length 239;
Best Local Similarity 24.4%; Pred. No. 2.6e+02;
RESULT 823
ID AAB12913 standard; protein; 239 AA.
DE Anti-human Fas immunoglobulin M light chain protein sequence SEQ ID #78.
PN JP2000154149-A.
PD 06-JUN-2000.
PA (SANY ) SANKYO CO LTD.
Query Match 6.6%; Score 68; DB 3; Length 239;
Best Local Similarity 24.4%; Pred. No. 2.6e+02;
RESULT 824
ID AAB12915 standard; protein; 239 AA.
DE Anti-human Fas immunoglobulin M light chain protein sequence SEQ ID #82.
PN JP2000154149-A.
PD 06-JUN-2000.
PA (SANY ) SANKYO CO LTD.
Query Match 6.6%; Score 68; DB 3; Length 239;
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Best Local Similarity 24.4%; Pred. No. 2.6e+02;
RESULT 825
ID AAG85024 standard; protein; 281 AA.
DE Shrimp white spot Bacilliform virus (WSBV) protein 115.
PN WO200138351-A2.
PD 31-MAY-2001.
PA (PENY-) PE CORP NY.
PA (THIR-) THIRD INST OCEANOGRAPHY STATE OCEANI C A.
PA (SINO-) SINOGENOMAX CO LTD.
Query Match 6.6%; Score 68; DB 4; Length 281;
Best Local Similarity 18.5%; Pred. No. 3.2e+02;
RESULT 826
ID ABB50152 standard; protein; 284 AA.
DE Human transcription factor TRFX-3.
PN WO200172777-A2.
PD 04-OCT-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.6%; Score 68; DB 4; Length 284;
Best Local Similarity 22.6%; Pred. No. 3.3e+02;
RESULT 827
ID AAG20023 standard; protein; 290 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 22048.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.6%; Score 68; DB 3; Length 290;
Best Local Similarity 26.7%; Pred. No. 3.4e+02;
RESULT 828
ID AAG54068 standard; protein; 290 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68900.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.6%; Score 68; DB 3; Length 290;
Best Local Similarity 26.7%; Pred. No. 3.4e+02;
RESULT 829
ID AAG20022 standard; protein; 297 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 22047.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.6%; Score 68; DB 3; Length 297;
Best Local Similarity 26.7%; Pred. No. 3.5e+02;
RESULT 830
ID AAG54067 standard; protein; 297 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68899.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.6%; Score 68; DB 3; Length 297;
Best Local Similarity 26.7%; Pred. No. 3.5e+02;
RESULT 831
ID AAB92505 standard; protein; 312 AA.
DE Human protein sequence SEQ ID NO: 10623.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 6.6%; Score 68; DB 4; Length 312;
Best Local Similarity 22.6%; Pred. No. 3.7e+02;
RESULT 832
ID ABB61033 standard; protein; 319 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 9891.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEXE-) PE CORP NY.
Query Match 6.6%; Score 68; DB 4; Length 319;
Best Local Similarity 23.1%; Pred. No. 3.8e+02;
RESULT 833
ID AAU17350 standard; protein; 381 AA.
DE Novel signal transduction pathway protein, Seq ID 915.
PN WO200154733-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.6%; Score 68; DB 4; Length 381;
Best Local Similarity 21.1%; Pred. No. 4.9e+02;
RESULT 834
ID ADB94058 standard; protein; 381 AA.
DE Human novel protein #292.
PN US2002168711-A1.
PD 14-NOV-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 6.6%; Score 68; DB 7; Length 381;
Best Local Similarity 21.1%; Pred. No. 4.9e+02;
RESULT 835
ID ADRI0385 standard; protein; 403 AA.
DE Human protein useful for treating neurological disease Seq 3891.
PN EP1474713-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.6%; Score 68; DB 8; Length 403;
Best Local Similarity 24.2%; Pred. No. 5.3e+02;
RESULT 836
ID AAG31616 standard; protein; 440 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 37997.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.6%; Score 68; DB 3; Length 440;
Best Local Similarity 21.7%; Pred. No. 6e+02;
RESULT 837
ID ADE52656 standard; protein; 461 AA.
DE Murine dhaform34196, SEQ ID 22.
PN WO2003089466-A1.
PD 30-OCT-2003.
PA (RIKE-) RIKEN KK.
PA (DNAF-) DNAFORM KK.
PA (MITU-) MITSUBISHI CHEM CORP.
Query Match 6.6%; Score 68; DB 8; Length 461;
Best Local Similarity 23.1%; Pred. No. 6.4e+02;
RESULT 838
ID AAG75628 standard; protein; 472 AA.
DE Human colon cancer antigen protein SEQ ID NO: 6392.
PN WO200122920-A2.
PD 05-APR-2001.
Query Match 6.6%; Score 68; DB 4; Length 472;
Best Local Similarity 24.3%; Pred. No. 6.6e+02;
RESULT 839
ID ADR86125 standard; protein; 480 AA.
DE Aspergillus fumigatus essential gene protein #175.
PN WO2004067709-A2.
PD 12-AUG-2004.
PA (ELIT-) ELITRA PHARM INC.
PA (ELIT-) ELITRA CANADA LTD.
Query Match 6.6%; Score 68; DB 8; Length 480;
Best Local Similarity 25.0%; Pred. No. 6.7e+02;
RESULT 840
ID ABG28970 standard; protein; 489 AA.
DE Novel human diagnostic protein #28961.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.6%; Score 68; DB 4; Length 489;
Best Local Similarity 29.7%; Pred. No. 6.9e+02;
RESULT 841
ID ADB63899 standard; protein; 504 AA.
DE Human protein encoded by clone BRACE20003310.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.6%; Score 68; DB 7; Length 504;
Best Local Similarity 24.6%; Pred. No. 7.2e+02;
RESULT 842
ID AAG31615 standard; protein; 505 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 37996.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.6%; Score 68; DB 3; Length 505;
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Best Local Similarity 21.7%; Pred. No. 7.2e+02;
RESULT 843
ID ADB08399 standard; protein; 520 AA.
DE Novel protein (useful for identifying genetic disorders) #554.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 6.6%; Score 68; DB 7; Length 520;
Best Local Similarity 31.7%; Pred. No. 7.5e+02;
RESULT 844
ID ADI60242 standard; protein; 520 AA.
DE Secreted polypeptide #126.
PN WO2003025142-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 6.6%; Score 68; DB 7; Length 520;
Best Local Similarity 22.5%; Pred. No. 7.5e+02;
RESULT 845
ID AAG31614 standard; protein; 522 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 37995.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.6%; Score 68; DB 3; Length 522;
Best Local Similarity 21.7%; Pred. No. 7.6e+02;
RESULT 846
ID AAE30008 standard; protein; 537 AA.
DE Tobacco cytochrome P450 protein, CYP73A27.
PN WO200272758-A2.
PD 19-SEP-2002.
PA (KENT) UNIV KENTUCKY RES FOUND.
Query Match 6.6%; Score 68; DB 6; Length 537;
Best Local Similarity 25.8%; Pred. No. 7.9e+02;
RESULT 847
ID ABM85497 standard; protein; 564 AA.
DE Human protein sequence hCP43333.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGE-) SAGES DISCOVERY.
Query Match 6.6%; Score 68; DB 7; Length 564;
Best Local Similarity 24.2%; Pred. No. 8.4e+02;
RESULT 848
ID AAW41418 standard; protein; 591 AA.
DE Paxillin beta isoform.
PN EP818533-A2.
PD 14-JAN-1998.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 6.6%; Score 68; DB 2; Length 591;
Best Local Similarity 24.2%; Pred. No. 9e+02;
RESULT 849
ID AAM39498 standard; protein; 600 AA.
DE Human polypeptide SEQ ID NO 2643.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.6%; Score 68; DB 4; Length 600;
Best Local Similarity 21.1%; Pred. No. 9.1e+02;
RESULT 850
ID AAB15251 standard; protein; 600 AA.
DE Human RNA metabolism protein-14 (RMEP-14).
PN WO200183524-A2.
PD 08-NOV-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.6%; Score 68; DB 5; Length 600;
Best Local Similarity 21.1%; Pred. No. 9.1e+02;
RESULT 851
ID ABB89510 standard; protein; 600 AA.
DE Human polypeptide SEQ ID NO 1886.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.6%; Score 68; DB 5; Length 600;
Best Local Similarity 21.1%; Pred. No. 9.1e+02;
RESULT 852

ID AAM41419 standard; protein; 605 AA.
DE Paxillin gamma isoform.
PN EP818533-A2.
PD 14-JAN-1998.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 6.6%; Score 68; DB 2; Length 605;
Best Local Similarity 24.2%; Pred. No. 9.2e+02;
RESULT 853
ID ADA55124 standard; protein; 606 AA.
DE Human protein, SEQ ID 2692.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.6%; Score 68; DB 6; Length 606;
Best Local Similarity 21.1%; Pred. No. 9.3e+02;
RESULT 854
ID ABM83699 standard; protein; 608 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3948.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.6%; Score 68; DB 8; Length 608;
Best Local Similarity 24.2%; Pred. No. 9.3e+02;
RESULT 855
ID AAB42369 standard; protein; 613 AA.
DE Human ORFX ORP2133 polypeptide sequence SEQ ID NO:4266.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 6.6%; Score 68; DB 3; Length 613;
Best Local Similarity 21.1%; Pred. No. 9.4e+02;
RESULT 856
ID AAM79654 standard; protein; 615 AA.
DE Human protein SEQ ID NO 3300.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.6%; Score 68; DB 4; Length 615;
Best Local Similarity 21.1%; Pred. No. 9.5e+02;
RESULT 857
ID AAM41284 standard; protein; 615 AA.
DE Human polypeptide SEQ ID NO 6215.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.6%; Score 68; DB 4; Length 615;
Best Local Similarity 21.1%; Pred. No. 9.5e+02;
RESULT 858
ID ADB84598 standard; protein; 619 AA.
DE Human mitogen-activated protein kinase kinase 2.3 (MEKK2.3).
PN US2003064496-A1.
PD 03-APR-2003.
PA (ATHE-) ATHEROGENICS INC.
Query Match 6.6%; Score 68; DB 7; Length 619;
Best Local Similarity 20.9%; Pred. No. 9.5e+02;
RESULT 859
ID ADK68587 standard; protein; 619 AA.
DE Human MEKK2.3 protein.
PN US2004019918-A1.
PD 29-JAN-2004.
PA (ATHE-) ATHEROGENICS INC.
Query Match 6.6%; Score 68; DB 8; Length 619;
Best Local Similarity 20.9%; Pred. No. 9.5e+02;
RESULT 860
ID ADM48232 standard; protein; 621 AA.
DE Polypeptide sequence #282 useful in producing transgenic plants.
PN US2003233670-A1.
PD 18-DEC-2003.
PA (EDGE/) EDGERTON M D.
PA (CHOM/) CHOMET P S.
PA (LACC/) LACCETTI L B.
Query Match 6.6%; Score 68; DB 8; Length 621;

Best Local Similarity 26.9%; Pred. No. 9.6e+02;
RESULT 861
ID AAM78670 standard; protein; 622 AA.
DE Human protein SEQ ID NO 1332.
PN WO200157190-A2.
PA (HYSE-) HYSEQ INC. 6.6%; Score 68; DB 4; Length 622;
Query Match 21.1%; Pred. No. 9.6e+02;
Best Local Similarity 21.1%; Pred. No. 9.6e+02;
RESULT 862
ID ABM83701 standard; protein; 639 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3950.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP. 6.6%; Score 68; DB 8; Length 639;
Query Match 24.2%; Pred. No. 1e+03;
Best Local Similarity 24.2%; Pred. No. 1e+03;
RESULT 863
ID ABM83698 standard; protein; 642 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3947.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP. 6.6%; Score 68; DB 8; Length 642;
Query Match 24.2%; Pred. No. 1e+03;
Best Local Similarity 24.2%; Pred. No. 1e+03;
RESULT 864
ID ABM83697 standard; protein; 645 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3946.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP. 6.6%; Score 68; DB 8; Length 645;
Query Match 24.2%; Pred. No. 1e+03;
Best Local Similarity 24.2%; Pred. No. 1e+03;
RESULT 865
ID AAY09004 standard; protein; 647 AA.
DE Wheat starch soluble synthase I (SSS I) amino acid sequence.
PN WO9914314-A1.
PD 25-MAR-1999.
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
PA (AUSU) UNIV AUSTRALIAN NAT.
PA (GOOD-) GOODMAN FIELDER LTD.
PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.
Query Match 6.6%; Score 68; DB 2; Length 647;
Best Local Similarity 24.6%; Pred. No. 1e+03;
RESULT 866
ID ABM83700 standard; protein; 668 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3949.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP. 6.6%; Score 68; DB 8; Length 668;
Query Match 24.2%; Pred. No. 1.1e+03;
Best Local Similarity 24.2%; Pred. No. 1.1e+03;
RESULT 867
ID AAW23937 standard; protein; 671 AA.
DE Wheat soluble starch synthase partial sequence.
PN WO9745545-A1.
PD 04-DEC-1997.
PA (AGRE) HOECHST-SCHERING AGREVO GMBH.
Query Match 6.6%; Score 68; DB 2; Length 671;
Best Local Similarity 24.6%; Pred. No. 1.1e+03;
RESULT 868
ID ADM87221 standard; protein; 681 AA.
DE Human protein SEQ ID NO:314.
PN WO2004009834-A2.
PD 29-JAN-2004.
PA (NUVE-) NUVELO INC. 6.6%; Score 68; DB 8; Length 681;
Query Match 24.0%; Pred. No. 1.1e+03;
Best Local Similarity 24.0%; Pred. No. 1.1e+03;
RESULT 869
ID ADJ68493 standard; protein; 691 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID299.
PN WO2003087768-A2.
PD 23-OCT-2003.

PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 6.6%; Score 68; DB 7; Length 691;
Best Local Similarity 27.2%; Pred. No. 1.1e+03;
RESULT 870
ID AAY50818 standard; protein; 756 AA.
DE Wheat soluble starch synthase protein.
PN DE19820607-A1.
PD 11-NOV-1999.
PA (AGRE) HOECHST-SCHERING AGREVO GMBH.
Query Match 6.6%; Score 68; DB 3; Length 756;
Best Local Similarity 24.6%; Pred. No. 1.3e+03;
RESULT 871
ID AAG65887 standard; protein; 897 AA.
DE Amino acid sequence of GSK gene Id 14936.
PN WO200172961-A2.
PD 04-OCT-2001.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 6.6%; Score 68; DB 4; Length 897;
Best Local Similarity 22.3%; Pred. No. 1.6e+03;
RESULT 872
ID ABG27877 standard; protein; 897 AA.
DE Novel human diagnostic protein #27868.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC. 6.6%; Score 68; DB 4; Length 897;
Query Match 27.2%; Pred. No. 1.6e+03;
Best Local Similarity 27.2%; Pred. No. 1.6e+03;
RESULT 873
ID ABG06309 standard; protein; 897 AA.
DE Novel human diagnostic protein #6300.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC. 6.6%; Score 68; DB 4; Length 897;
Query Match 22.3%; Pred. No. 1.6e+03;
Best Local Similarity 22.3%; Pred. No. 1.6e+03;
RESULT 874
ID ABG91402 standard; protein; 897 AA.
DE Primate LP283.
PN WO200263009-A2.
PD 15-AUG-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 6.6%; Score 68; DB 5; Length 897;
Best Local Similarity 22.3%; Pred. No. 1.6e+03;
RESULT 875
ID ADE07852 standard; protein; 897 AA.
DE Novel protein (useful for identifying genetic disorders) #7.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC. 6.6%; Score 68; DB 7; Length 897;
Query Match 22.3%; Pred. No. 1.6e+03;
Best Local Similarity 22.3%; Pred. No. 1.6e+03;
RESULT 876
ID ADE08940 standard; protein; 897 AA.
DE Novel protein-related contig polypeptide sequence #6.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC. 6.6%; Score 68; DB 7; Length 897;
Query Match 22.3%; Pred. No. 1.6e+03;
Best Local Similarity 22.3%; Pred. No. 1.6e+03;
RESULT 877
ID AAG67393 standard; protein; 1244 AA.
DE Amino acid sequence of human protein kinase SGK223.
PN WO200166594-A2.
PD 13-SEP-2001.
PA (SUGE-) SUGEN INC. 6.6%; Score 68; DB 4; Length 1244;
Query Match 24.0%; Pred. No. 2.5e+03;
Best Local Similarity 24.0%; Pred. No. 2.5e+03;
RESULT 878
ID AAE32023 standard; protein; 1406 AA.
DE Human kinase and phosphatase (KPP)-4.
PN WO200283709-A2.

PD 24-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.5%; Score 68; DB 6; Length 1406;
Best Local Similarity 24.0%; Pred. No. 2.9e+03;
RESULT 879
ID ABO85004 standard; protein; 2527 AA.
DE Murine cancer-associated protein (CAP) MP07-106.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 6.6%; Score 68; DB 8; Length 2527;
Best Local Similarity 30.6%; Pred. No. 6.5e+03;
RESULT 880
ID ABG10779 standard; protein; 150 AA.
DE Novel human diagnostic protein #10770.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.5%; Score 67.5; DB 4; Length 150;
Best Local Similarity 26.0%; Pred. No. 1.5e+02;
RESULT 881
ID ABP73640 standard; protein; 181 AA.
DE Candida albicans essential protein SEQ ID NO 7477.
PN WO200253728-A2.
PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.5%; Score 67.5; DB 5; Length 181;
Best Local Similarity 25.2%; Pred. No. 2e+02;
RESULT 882
ID ADR09724 standard; protein; 267 AA.
DE Human protein useful for treating neurological disease Seq 3230.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.5%; Score 67.5; DB 8; Length 267;
Best Local Similarity 22.8%; Pred. No. 3.4e+02;
RESULT 883
ID AAU45724 standard; protein; 268 AA.
DE Propionibacterium acnes immunogenic protein #6620.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 6.5%; Score 67.5; DB 4; Length 268;
Best Local Similarity 24.5%; Pred. No. 3.4e+02;
RESULT 884
ID ABM42243 standard; protein; 268 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #6919.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 6.5%; Score 67.5; DB 6; Length 268;
Best Local Similarity 24.5%; Pred. No. 3.4e+02;
RESULT 885
ID AAE01515 standard; protein; 329 AA.
DE Human gene 1 encoded secreted protein fragment, SEQ ID NO:172.
PN WO200134626-A1.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.5%; Score 67.5; DB 4; Length 329;
Best Local Similarity 26.0%; Pred. No. 4.5e+02;
RESULT 886
ID AAB32109 standard; protein; 362 AA.
DE Human secreted protein BLAST search protein SEQ ID NO: 167.
PN WO200058350-A1.
PD 05-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.5%; Score 67.5; DB 3; Length 362;
Best Local Similarity 21.2%; Pred. No. 5.2e+02;
RESULT 887
ID ABB60221 standard; protein; 380 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 7455.
PN WO200171042-A2.
PD 27-SEP-2001.

PA (PEKE) PE CORP NY.
Query Match 6.5%; Score 67.5; DB 4; Length 380;
Best Local Similarity 20.6%; Pred. No. 5.5e+02;
RESULT 888
ID ADI60126 standard; protein; 382 AA.
DE Secreted polypeptide #10.
PN WO2003025142-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 6.5%; Score 67.5; DB 7; Length 382;
Best Local Similarity 26.0%; Pred. No. 5.6e+02;
RESULT 889
ID AAO17422 standard; protein; 400 AA.
DE A thaliana hydroxyphenylpyruvate dioxygenase.
PN WO200231173-A2.
PD 18-APR-2002.
PA (SUNG-) SUNGENE GMBH & CO KGAA.
Query Match 6.5%; Score 67.5; DB 5; Length 400;
Best Local Similarity 25.0%; Pred. No. 5.9e+02;
RESULT 890
ID AAE29765 standard; protein; 415 AA.
DE Human fibulin-like protein mature protein.
PN WO200272138-A1.
PD 19-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 6.5%; Score 67.5; DB 6; Length 415;
Best Local Similarity 26.0%; Pred. No. 6.2e+02;
RESULT 891
ID AAU41941 standard; protein; 417 AA.
DE A. thaliana truncated p-hydroxyphenylpyruvate dioxygenase.
PN WO9749816-A1.
PD 31-DEC-1997.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 6.5%; Score 67.5; DB 2; Length 417;
Best Local Similarity 25.0%; Pred. No. 6.3e+02;
RESULT 892
ID AAE01436 standard; protein; 439 AA.
DE Human gene 1 encoded secreted protein HWLFJ10, SEQ ID NO:91.
PN WO200134626-A1.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.5%; Score 67.5; DB 4; Length 439;
Best Local Similarity 26.0%; Pred. No. 6.7e+02;
RESULT 893
ID AAE01464 standard; protein; 439 AA.
DE Human gene 1 encoded secreted protein HWLFJ10, SEQ ID NO:119.
PN WO200134626-A1.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.5%; Score 67.5; DB 4; Length 439;
Best Local Similarity 26.0%; Pred. No. 6.7e+02;
RESULT 894
ID AAG79415 standard; protein; 439 AA.
DE CADHP-4, Incyte ID No: 079370CD1.
PN WO200259312-A2.
PD 01-AUG-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.5%; Score 67.5; DB 5; Length 439;
Best Local Similarity 26.0%; Pred. No. 6.7e+02;
RESULT 895
ID ABG63881 standard; protein; 439 AA.
DE Human albumin fusion protein #556.
PN WO20017137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.5%; Score 67.5; DB 5; Length 439;
Best Local Similarity 26.0%; Pred. No. 6.7e+02;
RESULT 896
ID ABG63880 standard; protein; 439 AA.
DE Human albumin fusion protein #555.
PN WO20017137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

RESULT 913
ID AAU07837 standard; protein; 647 AA.
DE Amino acid sequence of human apoptin-associating filamin clone #1.
PN CA2290031-A1.
PD 06-JUN-2001.
PA (LEAD-) LEADD BV.
Query Match 6.5%; Score 67.5; DB 4; Length 647;
Best Local Similarity 21.2%; Pred. No. 1.1e+03;
RESULT 914
ID AAG78845 standard; protein; 647 AA.
DE Human apoptin-associating filamin clone protein #1.
PN JP2001178464-A.
PD 03-JUL-2001.
PA (LEAD-) LEADD BV.
Query Match 6.5%; Score 67.5; DB 4; Length 647;
Best Local Similarity 21.2%; Pred. No. 1.1e+03;
RESULT 915
ID ADH08343 standard; protein; 647 AA.
DE Human apoptin-associating protein #1.
PN US6520925-B1.
PD 16-SEP-2003.
PA (LEAD-) LEADD BV.
Query Match 6.5%; Score 67.5; DB 7; Length 647;
Best Local Similarity 21.2%; Pred. No. 1.1e+03;
RESULT 916
ID ADM05661 standard; protein; 705 AA.
DE Human protein of the invention SEQ ID NO:4346.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.5%; Score 67.5; DB 7; Length 705;
Best Local Similarity 22.0%; Pred. No. 1.3e+03;
RESULT 917
ID ADV76524 standard; protein; 743 AA.
DE Novel human secreted and transmembrane protein SeqID 198.
PN WO2003072035-A2.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 6.5%; Score 67.5; DB 7; Length 743;
Best Local Similarity 24.5%; Pred. No. 1.4e+03;
RESULT 918
ID AAY73351 standard; protein; 810 AA.
DE HTRM clone 1484257 protein sequence.
PN WO9957144-A2.
PD 11-NOV-1999.
PA (INCY-) INCYTE PHARM INC.
Query Match 6.5%; Score 67.5; DB 3; Length 810;
Best Local Similarity 23.1%; Pred. No. 1.6e+03;
RESULT 919
ID AAM40475 standard; protein; 817 AA.
DE Human polypeptide SEQ ID NO 5406.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.5%; Score 67.5; DB 4; Length 817;
Best Local Similarity 23.8%; Pred. No. 1.6e+03;
RESULT 920
ID ADQ30573 standard; protein; 838 AA.
DE Pancreas cancer marker - hypothetical 88.6 kDa protein.
PN WO2004055519-A2.
PD 01-JUL-2004.
PA (HOFF) HOPFMAN LA ROCHE & CO AG F.
PA (SINO-) SINOGENOMAX CO LTD CHINESE NAT HUMAN GEN.
Query Match 6.5%; Score 67.5; DB 8; Length 838;
Best Local Similarity 21.2%; Pred. No. 1.6e+03;
RESULT 921
ID ABG21022 standard; protein; 973 AA.
DE Novel human diagnostic protein #21013.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.5%; Score 67.5; DB 4; Length 973;
Best Local Similarity 20.5%; Pred. No. 2e+03;
RESULT 922
ID ABB64623 standard; protein; 989 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 20661.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.5%; Score 67.5; DB 4; Length 989;
Best Local Similarity 20.1%; Pred. No. 2e+03;
RESULT 923
ID ABU70541 standard; protein; 1036 AA.
DE Human adipocyte Selected Interacting domain, SID, #172.
PN WO200286122-A2.
PD 31-OCT-2002.
PA (HYBR-) HYBRIGENICS.
Query Match 6.5%; Score 67.5; DB 6; Length 1036;
Best Local Similarity 21.2%; Pred. No. 2.2e+03;
RESULT 924
ID ADE08476 standard; protein; 1334 AA.
DE Novel protein (useful for identifying genetic disorders) #631.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 6.5%; Score 67.5; DB 7; Length 1334;
Best Local Similarity 26.0%; Pred. No. 3.1e+03;
RESULT 925
ID ABG70209 standard; protein; 2608 AA.
DE Human prey protein for Shigella ipah9.8 #39.
PN WO200257303-A2.
PD 25-JUL-2002.
PA (HYBR-) HYBRIGENICS.
Query Match 6.5%; Score 67.5; DB 5; Length 2608;
Best Local Similarity 21.2%; Pred. No. 7.7e+03;
RESULT 926
ID AAW19349 standard; protein; 2647 AA.
DE Human filamin.
PN WO9725423-A1.
PD 17-JUL-1997.
PA (ICOS-) ICOS CORP.
Query Match 6.5%; Score 67.5; DB 2; Length 2647;
Best Local Similarity 21.2%; Pred. No. 7.9e+03;
RESULT 927
ID AAY33867 standard; protein; 2647 AA.
DE Carboxyl terminal of filamin, amino acid sequence.
PN US5948891-A.
PD 07-SEP-1999.
PA (ICOS-) ICOS CORP.
Query Match 6.5%; Score 67.5; DB 2; Length 2647;
Best Local Similarity 21.2%; Pred. No. 7.9e+03;
RESULT 928
ID ABR59725 standard; protein; 2647 AA.
DE Human filamin A alpha.
PN WO2003029277-A2.
PD 10-APR-2003.
PA (RIGE-) RIGEL PHARM INC.
Query Match 6.5%; Score 67.5; DB 6; Length 2647;
Best Local Similarity 21.2%; Pred. No. 7.9e+03;
RESULT 929
ID ADI82529 standard; protein; 2647 AA.
DE Human modifier of p21 (MP21) protein sequence SeqID95.
PN WO2004005486-A2.
PD 15-JAN-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 6.5%; Score 67.5; DB 8; Length 2647;
Best Local Similarity 21.2%; Pred. No. 7.9e+03;
RESULT 930
ID ADJ66545 standard; protein; 2647 AA.
DE Filamin A for anti-cancer protein complex.
PN WO2004009622-A2.
PD 29-JAN-2004.
PA (CELL-) CELLZONE AG.
Query Match 6.5%; Score 67.5; DB 8; Length 2647;
Best Local Similarity 21.2%; Pred. No. 7.9e+03;
RESULT 931

ID ADL35479 standard; protein; 2647 AA.
DE Human filamin A, alpha (actin-binding protein 280) (FLNA) protein.
PN WO2004019893-A2.
PD 11-MAR-2004.
PA (RIGE-) RIGEL PHARM INC.
Query Match 6.5%; Score 67.5; DB 8; Length 2647;
Best Local Similarity 21.2%; Pred. No. 7.9e+03;
RESULT 932
ID ADQ30522 standard; protein; 2647 AA.
DE Pancreas cancer marker - filamin A.
PN WO2004055519-A2.
PD 01-JUL-2004.
PA (HOPP) HOPPMANN LA ROCHE & CO AG F.
PA (SINO-) SINOGENOWAX CO LTD CHINESE NAT HUMAN GEN.
Query Match 6.5%; Score 67.5; DB 8; Length 2647;
Best Local Similarity 21.2%; Pred. No. 7.9e+03;
RESULT 933
ID ADS88205 standard; protein; 2647 AA.
DE Human protein of a TNF-alpha signalling pathway protein complex SeqID 60.
PN WO2004035783-A2.
PD 29-APR-2004.
PA (CELL-) CELLZOME AG.
Query Match 6.5%; Score 67.5; DB 8; Length 2647;
Best Local Similarity 21.2%; Pred. No. 7.9e+03;
RESULT 934
ID ABP76679 standard; protein; 19938 AA.
DE Streptomyces viridochromogenes Avi gene cluster polypeptide frame 3.
PN WO200268436-A1.
PD 06-SEP-2002.
PA (COMB-) COMBINATURE BIOPHARM AG.
Query Match 6.5%; Score 67.5; DB 6; Length 19938;
Best Local Similarity 23.2%; Pred. No. 1.2e+05;
RESULT 935
ID ABP64763 standard; protein; 39 AA.
DE Human protein SEQ ID 423.
PN WO200259260-A2.
PD 01-AUG-2002.
PA (HYSE-) HYSEQ INC.
Query Match 6.5%; Score 67; DB 5; Length 39;
Best Local Similarity 33.3%; Pred. No. 28;
RESULT 936
ID AA013689 standard; protein; 65 AA.
DE Human polypeptide SEQ ID NO 27581.
PN WO200184835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.5%; Score 67; DB 4; Length 65;
Best Local Similarity 25.3%; Pred. No. 55;
RESULT 937
ID AAW22490 standard; protein; 111 AA.
DE Phaffia derived glyceraldehyde-3-phosphate dehydrogenase PRCDNA68.
PN WO9723633-A1.
PD 03-JUL-1997.
PA (KONN) GIST-BROCADES BV.
PA (OOLJ/) OOLJEN A J J.
Query Match 6.5%; Score 67; DB 2; Length 111;
Best Local Similarity 31.2%; Pred. No. 1.2e+02;
RESULT 938
ID AAU16548 standard; protein; 136 AA.
DE Human novel secreted protein, Seq ID 1501.
PN WO200155322-A2.
PD 02-AUG-2001.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 6.5%; Score 67; DB 4; Length 136;
Best Local Similarity 25.6%; Pred. No. 1.5e+02;
RESULT 939
ID ABU55617 standard; protein; 136 AA.
DE Human novel polypeptide #704.
PN US2002132753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.

Query Match 6.5%; Score 67; DB 6; Length 136;
Best Local Similarity 25.6%; Pred. No. 1.5e+02;
RESULT 940
ID ADR19323 standard; protein; 219 AA.
DE Murine IgG1 light chain antibody (kappa chain), mIgG-Pankol.
PN WO2004065423-A2.
PD 05-AUG-2004.
PA (NEMO-) NEMOD BIOTHERAPEUTICS GMBH & CO KG.
Query Match 6.5%; Score 67; DB 8; Length 219;
Best Local Similarity 23.4%; Pred. No. 2.9e+02;
RESULT 941
ID AAE21131 standard; peptide; 229 AA.
DE Human clone HKrT1 zinc finger protein.
PN WO200208286-A2.
PD 31-JAN-2002.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 6.5%; Score 67; DB 5; Length 229;
Best Local Similarity 20.6%; Pred. No. 3.1e+02;
RESULT 942
ID AAE38670 standard; protein; 229 AA.
DE Zinc finger protein #9.
PN WO2003062455-A2.
PD 31-JUL-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 6.5%; Score 67; DB 7; Length 229;
Best Local Similarity 20.6%; Pred. No. 3.1e+02;
RESULT 943
ID ADQ75555 standard; protein; 288 AA.
DE Aplysia CCAAT-enhancer binding protein (ApC/EBP) short form.
PN KR2004019614-A.
PD 06-MAR-2004.
PA (UYSE-) UNIV SEOUL NAT IND FOUND.
Query Match 6.5%; Score 67; DB 8; Length 288;
Best Local Similarity 25.2%; Pred. No. 4.2e+02;
RESULT 944
ID ADP12406 standard; protein; 290 AA.
DE Protein encoded by mRNA of the invention #16.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 6.5%; Score 67; DB 8; Length 290;
Best Local Similarity 23.8%; Pred. No. 4.3e+02;
RESULT 945
ID ADQ87828 standard; protein; 290 AA.
DE Human CD16 alpha chain isotype A protein SEQ ID NO:1.
PN WO2004060052-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 6.5%; Score 67; DB 8; Length 290;
Best Local Similarity 23.8%; Pred. No. 4.3e+02;
RESULT 946
ID ABG91525 standard; protein; 297 AA.
DE Purine/pyrimidine triphosphate type nucleotidyltransferase #110.
PN WO200248331-A2.
PD 20-JUN-2002.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
Query Match 6.5%; Score 67; DB 5; Length 297;
Best Local Similarity 21.9%; Pred. No. 4.4e+02;
RESULT 947
ID ADS44722 standard; protein; 297 AA.
DE Bacterial polypeptide #23152.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.5%; Score 67; DB 8; Length 297;
Best Local Similarity 21.9%; Pred. No. 4.4e+02;
RESULT 948
ID ABB59585 standard; protein; 339 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 5547.

PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEXE) PE CORP NY.
Query Match 6.5%; Score 67; DB 4; Length 339;
Best Local Similarity 24.6%; Pred. No. 5.3e+02;
RESULT 949
ID ADQ75533 standard; protein; 340 AA.
DE Aplysia CCAAT-enhancer binding protein (ApC/EBP).
PN KR2004019614-A.
PD 06-MAR-2004.
PA (UYSE-) UNIV SEOUL NAT IND FOUND.
Query Match 6.5%; Score 67; DB 8; Length 340;
Best Local Similarity 25.2%; Pred. No. 5.3e+02;
RESULT 950
ID ADQ75554 standard; protein; 340 AA.
DE Aplysia CCAAT-enhancer binding protein (ApC/EBP) long form.
PN KR2004019614-A.
PD 06-MAR-2004.
PA (UYSE-) UNIV SEOUL NAT IND FOUND.
Query Match 6.5%; Score 67; DB 8; Length 340;
Best Local Similarity 25.2%; Pred. No. 5.3e+02;
RESULT 951
ID AAG39794 standard; protein; 344 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 49290.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.5%; Score 67; DB 3; Length 344;
Best Local Similarity 22.0%; Pred. No. 5.4e+02;
RESULT 952
ID AAU16126 standard; protein; 383 AA.
DE Human novel secreted protein, Seq ID 1079.
PN WO200155322-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.5%; Score 67; DB 4; Length 383;
Best Local Similarity 25.6%; Pred. No. 6.3e+02;
RESULT 953
ID ABUS5195 standard; protein; 383 AA.
DE Human novel polypeptide #282.
PN US2002132753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 6.5%; Score 67; DB 6; Length 383;
Best Local Similarity 25.6%; Pred. No. 6.3e+02;
RESULT 954
ID ABO69380 standard; protein; 385 AA.
DE Pseudomonas aeruginosa polypeptide #1555.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.5%; Score 67; DB 7; Length 385;
Best Local Similarity 23.5%; Pred. No. 6.3e+02;
RESULT 955
ID AAB94887 standard; protein; 392 AA.
DE Human protein sequence SEQ ID NO:16110.
PN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 6.5%; Score 67; DB 4; Length 392;
Best Local Similarity 21.1%; Pred. No. 6.5e+02;
RESULT 956
ID ADR08810 standard; protein; 392 AA.
DE Human protein useful for treating neurological disease Seq 2316.
PN EPI447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.5%; Score 67; DB 8; Length 392;
Best Local Similarity 21.1%; Pred. No. 6.5e+02;
RESULT 957
ID AAG39793 standard; protein; 411 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 49289.

PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.5%; Score 67; DB 3; Length 411;
Best Local Similarity 22.0%; Pred. No. 6.9e+02;
RESULT 958
ID AAG39792 standard; protein; 452 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 49288.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.5%; Score 67; DB 3; Length 452;
Best Local Similarity 22.0%; Pred. No. 7.9e+02;
RESULT 959
ID AAB95891 standard; protein; 479 AA.
DE Human protein sequence SEQ ID NO:19019.
PN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 6.5%; Score 67; DB 4; Length 479;
Best Local Similarity 21.9%; Pred. No. 8.5e+02;
RESULT 960
ID ADJ69992 standard; protein; 479 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1798.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 6.5%; Score 67; DB 7; Length 479;
Best Local Similarity 21.9%; Pred. No. 8.5e+02;
RESULT 961
ID AAE30009 standard; protein; 534 AA.
DE Tobacco cytochrome P450 protein, CYP73A28.
PN WO200272758-A2.
PD 19-SEP-2002.
PA (KENT) UNIV KENTUCKY RES FOUND.
Query Match 6.5%; Score 67; DB 6; Length 534;
Best Local Similarity 25.8%; Pred. No. 9.9e+02;
RESULT 962
ID ADR09496 standard; protein; 538 AA.
DE Human protein useful for treating neurological disease Seq 3002.
PN EPI447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.5%; Score 67; DB 8; Length 538;
Best Local Similarity 23.2%; Pred. No. 1e+03;
RESULT 963
ID AAY73345 standard; protein; 540 AA.
DE HTRM clone 438283 protein sequence.
PN WO9957144-A2.
PD 11-NOV-1999.
PA (INCY-) INCYTE PHARM INC.
Query Match 6.5%; Score 67; DB 3; Length 540;
Best Local Similarity 24.5%; Pred. No. 1e+03;
RESULT 964
ID ABM85496 standard; protein; 566 AA.
DE Mouse protein sequence mCP22058.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 6.5%; Score 67; DB 7; Length 566;
Best Local Similarity 24.2%; Pred. No. 1.1e+03;
RESULT 965
ID ABO58634 standard; protein; 587 AA.
DE Human genome derived single exon protein #4868.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 6.5%; Score 67; DB 8; Length 587;
Best Local Similarity 24.5%; Pred. No. 1.1e+03;
RESULT 966
ID ADA55036 standard; protein; 610 AA.
DE Human protein, SEQ ID 2604.

PN EPI293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.5%; Score 67; DB 6; Length 610;
Best Local Similarity 21.1%; Pred. No. 1.2e+03;
RESULT 967
ID ADM05087 standard; protein; 610 AA.
DE Human protein of the invention SEQ ID NO:3772.
PN EPI347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.5%; Score 67; DB 7; Length 610;
Best Local Similarity 21.1%; Pred. No. 1.2e+03;
RESULT 968
ID ADG10534 standard; protein; 616 AA.
DE Human therapeutic protein - SEQ ID 771.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 6.5%; Score 67; DB 8; Length 616;
Best Local Similarity 24.7%; Pred. No. 1.2e+03;
RESULT 969
ID ADG32339 standard; protein; 618 AA.
DE Fusion protein of AFP chitinase-scfV VD2 SeqID 48.
PN WO2003089475-A2.
PD 30-OCT-2003.
PA (FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.
Query Match 6.5%; Score 67; DB 7; Length 618;
Best Local Similarity 24.2%; Pred. No. 1.2e+03;
RESULT 970
ID ABG24363 standard; protein; 638 AA.
DE Novel human diagnostic protein #24354.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.5%; Score 67; DB 4; Length 638;
Best Local Similarity 22.4%; Pred. No. 1.3e+03;
RESULT 971
ID ABG08897 standard; protein; 638 AA.
DE Novel human diagnostic protein #8888.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.5%; Score 67; DB 4; Length 638;
Best Local Similarity 22.4%; Pred. No. 1.3e+03;
RESULT 972
ID ABG07106 standard; protein; 638 AA.
DE Novel human diagnostic protein #7097.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.5%; Score 67; DB 4; Length 638;
Best Local Similarity 22.4%; Pred. No. 1.3e+03;
RESULT 973
ID AAG67812 standard; protein; 640 AA.
DE Human zinc-finger protein 70.
PN CN1297903-A.
PD 06-JUN-2001.
PA (SHAN-) SHANGHAI BORONG GENE DEV CO LTD.
Query Match 6.5%; Score 67; DB 4; Length 640;
Best Local Similarity 25.6%; Pred. No. 1.3e+03;
RESULT 974
ID ADM06086 standard; protein; 666 AA.
DE Human protein of the invention SEQ ID NO:4771.
PN EPI347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.5%; Score 67; DB 7; Length 666;
Best Local Similarity 21.9%; Pred. No. 1.3e+03;
RESULT 975
ID ABU65208 standard; protein; 705 AA.
DE Human NOV120a protein.

PN WO200272757-A2.
PD 19-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 67; DB 5; Length 705;
Best Local Similarity 23.6%; Pred. No. 1.4e+03;
RESULT 976
ID ADN62067 standard; protein; 705 AA.
DE Human novel protein NOV120a.
PN US2004043382-A1.
PD 04-MAR-2004.
PA (PADI/) PADIGARU M.
PA (SPYT/) SPYTEK K A.
PA (SHEN/) SHENOY S G.
PA (TAUP/) TAUPIER R J.
PA (PENA/) PENA C E A.
PA (LILL/) LI L.
PA (ZERH/) ZERHUSEN B D.
PA (GUSE/) GUSEV V Y.
PA (JIWW/) JI W.
PA (GORM/) GORMAN L.
PA (MILL/) MILLER C E.
PA (KEKU/) KEKUDA R.
PA (PATT/) PATTURAJAN M.
PA (GANG/) GANGOLLI E A.
PA (VERN/) VERNET C A M.
PA (GUOX/) GUO X S.
PA (TCHE/) TCHERNEV V T.
PA (FERN/) FERNANDES E R.
PA (CASM/) CASMAN S J.
PA (MALY/) MALYANKAR U M.
PA (GERL/) GERLACH V.
PA (LIUY/) LIU Y.
PA (ANDE/) ANDERSON D W.
PA (SPAD/) SPADERNA S K.
PA (CATT/) CATTERTON E.
PA (LEIT/) LEITE M W.
PA (ZHON/) ZHONG H.
PA (ALSO/) ALSOBROOK J P.
PA (LEPL/) LEPLLEY D M.
PA (RIEG/) RIEGER D K.
PA (BURG/) BURGESS C E.
Query Match 6.5%; Score 67; DB 8; Length 705;
Best Local Similarity 23.6%; Pred. No. 1.4e+03;
RESULT 977
ID AAR68743 standard; protein; 706 AA.
DE BCL-6 zinc finger protein.
PN WO9429343-A1.
PD 22-DEC-1994.
PA (UYCO) UNIV COLUMBIA NEW YORK.
PA (SLOK) SLOAN KETTERING INST CANCER.
Query Match 6.5%; Score 67; DB 2; Length 706;
Best Local Similarity 22.3%; Pred. No. 1.5e+03;
RESULT 978
ID AAY78792 standard; protein; 706 AA.
DE Human BCL-6 protein sequence.
PN WO200000185-A1.
PD 06-JAN-2000.
PA (UYCO) UNIV COLUMBIA NEW YORK.
Query Match 6.5%; Score 67; DB 3; Length 706;
Best Local Similarity 22.3%; Pred. No. 1.5e+03;
RESULT 979
ID AAY78793 standard; protein; 706 AA.
DE Human BCL-6 protein sequence.
PN WO200000185-A1.
PD 06-JAN-2000.
PA (UYCO) UNIV COLUMBIA NEW YORK.
Query Match 6.5%; Score 67; DB 3; Length 706;
Best Local Similarity 22.3%; Pred. No. 1.5e+03;
RESULT 980
ID AAB29640 standard; protein; 706 AA.
DE Human bcl-6 transcriptional repressor.
PN US6140125-A.
PD 31-OCT-2000.

PA (ISIS-) ISIS PHARM INC.
Query Match 6.5%; Score 67; DB 4; Length 706;
Best Local Similarity 22.3%; Pred. No. 1.5e+03;
RESULT 981
ID ADJ70182 standard; protein; 706 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1988.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 6.5%; Score 67; DB 7; Length 706;
Best Local Similarity 22.3%; Pred. No. 1.5e+03;
RESULT 982
ID ADL82847 standard; protein; 706 AA.
DE Human PRO26296, SEQ ID 49.
PN WO2004024097-A2.
PD 25-MAR-2004.
PA (GETH-) GENENTECH INC.
Query Match 6.5%; Score 67; DB 8; Length 706;
Best Local Similarity 22.3%; Pred. No. 1.5e+03;
RESULT 983
ID ADRI4017 standard; protein; 706 AA.
DE Human NF-kappaB pathway-associated protein SeqID18.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.
Query Match 6.5%; Score 67; DB 8; Length 706;
Best Local Similarity 22.3%; Pred. No. 1.5e+03;
RESULT 984
ID ADRI4065 standard; protein; 706 AA.
DE Human NF-kappaB pathway-associated protein SeqID66.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.
Query Match 6.5%; Score 67; DB 8; Length 706;
Best Local Similarity 22.3%; Pred. No. 1.5e+03;
RESULT 985
ID ABB57289 standard; protein; 707 AA.
DE Mouse ischaemic condition related protein sequence SEQ ID NO:814.
PN WO200188188-A2.
PD 22-NOV-2001.
PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
Query Match 6.5%; Score 67; DB 5; Length 707;
Best Local Similarity 22.3%; Pred. No. 1.5e+03;
RESULT 986
ID ADA55078 standard; protein; 725 AA.
DE Human protein, SEQ ID 2646.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.5%; Score 67; DB 6; Length 725;
Best Local Similarity 24.7%; Pred. No. 1.5e+03;
RESULT 987
ID ADA55624 standard; protein; 733 AA.
DE Human protein, SEQ ID 3192.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.5%; Score 67; DB 6; Length 733;
Best Local Similarity 25.6%; Pred. No. 1.5e+03;
RESULT 988
ID ADJ68934 standard; protein; 738 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID740.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 6.5%; Score 67; DB 7; Length 738;
Best Local Similarity 21.1%; Pred. No. 1.5e+03;
RESULT 989
ID ABG07257 standard; protein; 896 AA.

DE Novel human diagnostic protein #7248.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.5%; Score 67; DB 4; Length 896;
Best Local Similarity 21.1%; Pred. No. 2e+03;
RESULT 990
ID ADJ69193 standard; protein; 995 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID999.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 6.5%; Score 67; DB 7; Length 995;
Best Local Similarity 25.6%; Pred. No. 2.3e+03;
RESULT 991
ID ABU48630 standard; protein; 1047 AA.
DE Protein encoded by Prokaryotic essential gene #34157.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.5%; Score 67; DB 6; Length 1047;
Best Local Similarity 25.4%; Pred. No. 2.5e+03;
RESULT 992
ID ABE61414 standard; protein; 1143 AA.
DE Human Protein XP_046094, SEQ ID NO 7333.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GHEO-) GEN HOSPITAL CORP.
PA (FARB-) BAYER AG.
Query Match 6.5%; Score 67; DB 7; Length 1143;
Best Local Similarity 25.6%; Pred. No. 2.8e+03;
RESULT 993
ID ADO23717 standard; protein; 1219 AA.
DE Nup153 related protein, SEQ ID 6.
PN WO2004027381-A2.
PD 01-APR-2004.
PA (UTAH-) UNIV UTAH RES FOUND.
Query Match 6.5%; Score 67; DB 8; Length 1219;
Best Local Similarity 26.5%; Pred. No. 3.1e+03;
RESULT 994
ID AAR79475 standard; protein; 1251 AA.
DE Mouse LTBP-3.
PN WO9522611-A2.
PD 24-AUG-1995.
PA (UNMI-) UNIV MICHIGAN.
Query Match 6.5%; Score 67; DB 2; Length 1251;
Best Local Similarity 22.9%; Pred. No. 3.2e+03;
RESULT 995
ID AAB61481 standard; protein; 1251 AA.
DE Murine LTBP-3 protein.
PN WO200100672-A1.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 6.5%; Score 67; DB 4; Length 1251;
Best Local Similarity 22.9%; Pred. No. 3.2e+03;
RESULT 996
ID AAB61483 standard; protein; 1251 AA.
DE Human TANGO 300 extracellular domain.
PN WO200100672-A1.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 6.5%; Score 67; DB 4; Length 1251;
Best Local Similarity 22.9%; Pred. No. 3.2e+03;
RESULT 997
ID AAB12271 standard; protein; 1253 AA.
DE Mouse Latent TGF-beta binding protein-3 (LTBP-3).
PN US6074840-A.
PD 13-JUN-2000.
PA (UNMI-) UNIV MICHIGAN.
Query Match 6.5%; Score 67; DB 3; Length 1253;
Best Local Similarity 22.9%; Pred. No. 3.2e+03;
RESULT 998
ID ABB07257 standard; protein; 896 AA.

ID AAB61420 standard; protein; 1253 AA.
DE Murine TANGO 275 protein.
FN WO200100672-A1.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 6.5%; Score 67; DB 4; Length 1253;
Best Local Similarity 22.9%; Pred. No. 3.2e+03;
RESULT 999
ID ADR31649 standard; protein; 1253 AA.
DE Murine latent transforming growth factor beta protein-3 (LTBP-3).
FN US6774105-B1.
PD 10-AUG-2004.
PA (UNMI) UNIV MICHIGAN.
Query Match 6.5%; Score 67; DB 8; Length 1253;
Best Local Similarity 22.9%; Pred. No. 3.2e+03;
RESULT 1000
ID AAE31481 standard; protein; 1287 AA.
DE Human B7-H1.2 partial splice variant protein #2.
FN WO200279474-A2.
PD 10-OCT-2002.
PA (IMMV) IMMUNEX CORP.
Query Match 6.5%; Score 67; DB 6; Length 1287;
Best Local Similarity 21.9%; Pred. No. 3.3e+03;
RESULT 1001
ID ADC71568 standard; protein; 1548 AA.
DE Mouse subtilisin-like protein convertase 6 (SPC6).
FN US2003093824-A1.
PD 15-MAY-2003.
PA (ALLE/) ALLEN K D.
Query Match 6.5%; Score 67; DB 7; Length 1548;
Best Local Similarity 20.9%; Pred. No. 4.2e+03;
RESULT 1002
ID ABG17466 standard; protein; 1655 AA.
DE Novel human diagnostic protein #17457.
FN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.5%; Score 67; DB 4; Length 1655;
Best Local Similarity 22.1%; Pred. No. 4.7e+03;
RESULT 1003
ID ABB80243 standard; protein; 1877 AA.
DE Murine subtilase.
FN WO2003060109-A2.
PD 24-JUL-2003.
PA (FARB) BAYER AG.
Query Match 6.5%; Score 67; DB 7; Length 1877;
Best Local Similarity 20.9%; Pred. No. 5.5e+03;
RESULT 1004
ID AAR12609 standard; protein; 2409 AA.
DE Versican.
FN WO9108230-A.
PD 13-JUN-1991.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
Query Match 6.5%; Score 67; DB 2; Length 2409;
Best Local Similarity 24.3%; Pred. No. 7.8e+03;
RESULT 1005
ID ABR47429 standard; protein; 2409 AA.
DE Breast cancer associated protein sequence SEQ ID NO:90.
FN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 6.5%; Score 67; DB 6; Length 2409;
Best Local Similarity 24.3%; Pred. No. 7.8e+03;
RESULT 1006
ID ADQ39514 standard; protein; 2409 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1177.
FN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 6.5%; Score 67; DB 8; Length 2409;
Best Local Similarity 24.3%; Pred. No. 7.8e+03;
RESULT 1007

ID ADQ39512 standard; protein; 2409 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1175.
FN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 6.5%; Score 67; DB 8; Length 2409;
Best Local Similarity 24.3%; Pred. No. 7.8e+03;
RESULT 1008
ID ADJ70171 standard; protein; 3024 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1977.
FN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 6.5%; Score 67; DB 7; Length 3024;
Best Local Similarity 24.3%; Pred. No. 1.1e+04;
RESULT 1009
ID ADD48597 standard; protein; 3396 AA.
DE Human Protein P13611, SEQ ID NO 14303.
FN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.5%; Score 67; DB 7; Length 3396;
Best Local Similarity 24.3%; Pred. No. 1.2e+04;
RESULT 1010
ID ADN95526 standard; protein; 3396 AA.
DE Human BEC/LEC-related protein sequence SeqID4449.
FN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 6.5%; Score 67; DB 7; Length 3396;
Best Local Similarity 24.3%; Pred. No. 1.2e+04;
RESULT 1011
ID ADJ75521 standard; protein; 3396 AA.
DE Marker gene related amino acid sequence SEQ ID NO:773.
FN EPI394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 6.5%; Score 67; DB 8; Length 3396;
Best Local Similarity 24.3%; Pred. No. 1.2e+04;
RESULT 1012
ID ADQ39509 standard; protein; 3396 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1172.
FN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 6.5%; Score 67; DB 8; Length 3396;
Best Local Similarity 24.3%; Pred. No. 1.2e+04;
RESULT 1013
ID ADQ39510 standard; protein; 3396 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1173.
FN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 6.5%; Score 67; DB 8; Length 3396;
Best Local Similarity 24.3%; Pred. No. 1.2e+04;
RESULT 1014
ID ADR99164 standard; protein; 3396 AA.
DE Chondroitin sulfate proteoglycan 2 (versican), CSPG2, SEQ ID 170.
FN WO2004078035-A2.
PD 16-SEP-2004.
PA (FARB) BAYER PHARM CORP.
Query Match 6.5%; Score 67; DB 8; Length 3396;
Best Local Similarity 24.3%; Pred. No. 1.2e+04;
RESULT 1015
ID ABP07937 standard; protein; 105 AA.
DE Human OREF protein sequence SEQ ID NO:15856.
FN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match 6.4%; Score 66.5; DB 5; Length 105;

Best Local Similarity 33.3%; Pred. No. 1.2e+02;
RESULT 1016
ID ABG08070 standard; protein; 197 AA.
DE Novel human diagnostic protein #8061.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 66.5; DB 4; Length 197;
Best Local Similarity 27.9%; Pred. No. 2.8e+02;
RESULT 1017
ID ABG11886 standard; protein; 218 AA.
DE Novel human diagnostic protein #11877.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 66.5; DB 4; Length 218;
Best Local Similarity 20.8%; Pred. No. 3.3e+02;
RESULT 1018
ID ABP51402 standard; protein; 250 AA.
DE Human MDDT SEQ ID NO 424.
PN WO200240715-A2.
PD 23-MAY-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.4%; Score 66.5; DB 5; Length 250;
Best Local Similarity 22.7%; Pred. No. 3.9e+02;
RESULT 1019
ID AAR63461 standard; protein; 257 AA.
DE Deduced AA sequence of UL49 homologue gene of BHV-1.
PN WO9424296-A2.
PD 27-OCT-1994.
PA (UYSA-) UNIV SASKATCHEWAN.
Query Match 6.4%; Score 66.5; DB 2; Length 257;
Best Local Similarity 23.7%; Pred. No. 4.1e+02;
RESULT 1020
ID AAB07662 standard; protein; 258 AA.
DE Amino acid sequence of the UL49 gene homologue of BHV-1.
PN US6086902-A.
PD 11-JUL-2000.
PA (UYSA-) UNIV SASKATCHEWAN.
Query Match 6.4%; Score 66.5; DB 3; Length 258;
Best Local Similarity 23.7%; Pred. No. 4.1e+02;
RESULT 1021
ID AAU11367 standard; protein; 258 AA.
DE Bovine herpesvirus protein.
PN US6316252-B1.
PD 13-NOV-2001.
PA (WISC-) WISCONSIN ALUMNI RES FOUND.
Query Match 6.4%; Score 66.5; DB 5; Length 258;
Best Local Similarity 23.7%; Pred. No. 4.1e+02;
RESULT 1022
ID ADG73120 standard; protein; 293 AA.
DE Pseudomonas syringae pv. tomato DC3000 Avr/Hop protein #57.
PN US2003204868-A1.
PD 30-OCT-2003.
PA (COLL-) COLIMER A.
PA (ALFA-) ALFANO J R.
PA (CART-) CARTINHOOR S W.
PA (SCHN-) SCHNEIDER D J.
PA (TANG-) TANG X.
Query Match 6.4%; Score 66.5; DB 7; Length 293;
Best Local Similarity 21.1%; Pred. No. 4.9e+02;
RESULT 1023
ID ADL12176 standard; protein; 293 AA.
DE Pseudomonas syringae anti-cancer protein #57.
PN WO2003068930-A2.
PD 21-AUG-2003.
PA (CORR-) CORNELL RES FOUND INC.
PA (USDA-) US SEC OF AGRIC.
PA (UYNE-) UNIV NEBRASKA.
PA (UNIV-) UNIV KANSAS STATE RES FOUND.
Query Match 6.4%; Score 66.5; DB 7; Length 293;
Best Local Similarity 21.1%; Pred. No. 4.9e+02;
RESULT 1024

ID ABB68531 standard; protein; 302 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 32385.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 6.4%; Score 66.5; DB 4; Length 302;
Best Local Similarity 22.1%; Pred. No. 5.1e+02;
RESULT 1025
ID AAG67815 standard; protein; 318 AA.
DE Human zinc-finger protein 35.
PN CN1297912-A.
PD 06-JUN-2001.
PA (SHAN-) SHANGHAI BORONG GENE DEV CO LTD.
Query Match 6.4%; Score 66.5; DB 4; Length 318;
Best Local Similarity 25.2%; Pred. No. 5.5e+02;
RESULT 1026
ID AAG64584 standard; protein; 345 AA.
DE Human zinc-finger protein 38.
PN CN1297917-A.
PD 06-JUN-2001.
PA (SHAN-) SHANGHAI BORONG GENE DEV CO LTD.
Query Match 6.4%; Score 66.5; DB 8; Length 353;
Best Local Similarity 26.1%; Pred. No. 6.3e+02;
RESULT 1028
ID ABF62906 standard; protein; 358 AA.
DE Human polypeptide SEQ ID NO 343.
PN WO200218424-A2.
PD 07-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 66.5; DB 5; Length 358;
Best Local Similarity 26.1%; Pred. No. 6.4e+02;
RESULT 1029
ID ADM05407 standard; protein; 407 AA.
DE Human protein of the invention SEQ ID NO:4092.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.4%; Score 66.5; DB 7; Length 407;
Best Local Similarity 26.1%; Pred. No. 7.7e+02;
RESULT 1030
ID AAB58777 standard; protein; 416 AA.
DE Breast and ovarian cancer associated antigen protein sequence SEQ ID 485.
PN WO200055173-A1.
PD 21-SEP-2000.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 6.4%; Score 66.5; DB 3; Length 416;
Best Local Similarity 21.2%; Pred. No. 7.9e+02;
RESULT 1031
ID ABU11528 standard; protein; 426 AA.
DE Human MDDT polypeptide SEQ ID 475.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.4%; Score 66.5; DB 6; Length 426;
Best Local Similarity 26.1%; Pred. No. 8.2e+02;
RESULT 1032
ID ADM30767 standard; protein; 437 AA.
DE Rat sonic hedgehog (SHH) polypeptide.
PN US2004072345-A1.
PD 15-APR-2004.
PA (ALTA-) ALTABA A R I.
PA (SANC-) SANCHEZ M P.
Query Match 6.4%; Score 66.5; DB 8; Length 437;
Best Local Similarity 26.1%; Pred. No. 8.2e+02;

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Best Local Similarity 23.4%; Pred. No. 8.5e+02;
RESULT 1033
ID ADO50491 standard; protein; 437 AA.
DE Rat sonic hedgehog (SHH) protein.
PN US2004092010-A1.
PD 13-MAY-2004.
PA (ALTA/) RUIZ I ALTABA A.
PA (ALVA/) ALVAREZ-BUYLLA A.
PA (LIND/) LIM D A.
PA (DAHM/) DAHMANE N.
PA (PALM/) PALMA V.
Query Match 6.4%; Score 66.5; DB 8; Length 437;
Best Local Similarity 23.4%; Pred. No. 8.5e+02;
RESULT 1034
ID ABG10471 standard; protein; 471 AA.
DE Novel human diagnostic protein #10462.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 66.5; DB 4; Length 471;
Best Local Similarity 23.7%; Pred. No. 9.4e+02;
RESULT 1035
ID ABU11515 standard; protein; 500 AA.
DE Human MDDT polypeptide SEQ ID 462.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.4%; Score 66.5; DB 6; Length 500;
Best Local Similarity 20.9%; Pred. No. 1e+03;
RESULT 1036
ID ADE31123 standard; protein; 500 AA.
DE Human diagnostic and therapeutic polypeptide (DITHP), SEQ ID NO 255.
PN WO2003062376-A2.
PD 31-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.4%; Score 66.5; DB 7; Length 500;
Best Local Similarity 20.9%; Pred. No. 1e+03;
RESULT 1037
ID ABR40852 standard; protein; 512 AA.
DE Glycine max oil trait related protein sequence SEQ ID NO:483.
PN WO2003002751-A2.
PD 09-JAN-2003.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 6.4%; Score 66.5; DB 6; Length 512;
Best Local Similarity 22.6%; Pred. No. 1.1e+03;
RESULT 1038
ID ABG91260 standard; protein; 546 AA.
DE C. albicans BAX-associated protein fragment SEQ ID 478.
PN WO200264766-A2.
PD 22-AUG-2002.
PA (JANC) JANSSEN PHARM NV.
Query Match 6.4%; Score 66.5; DB 5; Length 546;
Best Local Similarity 25.1%; Pred. No. 1.1e+03;
RESULT 1039
ID ABG93297 standard; protein; 546 AA.
DE C. albicans BAX-associated protein fragment SEQ ID 552.
PN WO200264766-A2.
PD 22-AUG-2002.
PA (JANC) JANSSEN PHARM NV.
Query Match 6.4%; Score 66.5; DB 5; Length 546;
Best Local Similarity 25.1%; Pred. No. 1.1e+03;
RESULT 1040
ID AAB95733 standard; protein; 569 AA.
DE Human protein sequence SEQ ID NO:18617.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 6.4%; Score 66.5; DB 4; Length 569;
Best Local Similarity 25.2%; Pred. No. 1.2e+03;
RESULT 1041
ID AAB95128 standard; protein; 569 AA.
DE Human protein sequence SEQ ID NO:17131.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 6.4%; Score 66.5; DB 4; Length 569;
Best Local Similarity 25.2%; Pred. No. 1.2e+03;
RESULT 1042
ID AAM51816 standard; protein; 582 AA.
DE Murine apoptase L100.
PN DE10019901-A1.
PD 25-OCT-2001.
PA (BADI) BASF-LYNK BIOSCIENCE AG.
Query Match 6.4%; Score 66.5; DB 4; Length 582;
Best Local Similarity 20.7%; Pred. No. 1.3e+03;
RESULT 1043
ID ADA54364 standard; protein; 588 AA.
DE Human protein, SEQ ID 1932.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
Query Match 6.4%; Score 66.5; DB 6; Length 588;
Best Local Similarity 20.9%; Pred. No. 1.3e+03;
RESULT 1044
ID ADJ80126 standard; protein; 588 AA.
DE Novel human nucleic acid-associated protein #2.
PN WO2003038052-A2.
PD 08-MAY-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.4%; Score 66.5; DB 7; Length 588;
Best Local Similarity 20.9%; Pred. No. 1.3e+03;
RESULT 1045
ID ADRI0375 standard; protein; 615 AA.
DE Human protein useful for treating neurological disease Seq 3881.
PN EP147413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.4%; Score 66.5; DB 8; Length 615;
Best Local Similarity 26.6%; Pred. No. 1.4e+03;
RESULT 1046
ID AAY06227 standard; protein; 647 AA.
DE Human filamin.
PN EP921192-A1.
PD 09-JUN-1999.
PA (LEAD-) LEADD BV.
Query Match 6.4%; Score 66.5; DB 2; Length 647;
Best Local Similarity 21.2%; Pred. No. 1.4e+03;
RESULT 1047
ID ADC31183 standard; protein; 701 AA.
DE Human novel contig-encoded polypeptide sequence, SEQ ID NO:3265.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 66.5; DB 7; Length 701;
Best Local Similarity 25.2%; Pred. No. 1.6e+03;
RESULT 1048
ID ABB63231 standard; protein; 764 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 16485.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.4%; Score 66.5; DB 4; Length 764;
Best Local Similarity 31.3%; Pred. No. 1.8e+03;
RESULT 1049
ID AAW81756 standard; protein; 803 AA.
DE Myc-binding zinc-finger protein.
PN EP875567-A2.
PD 04-NOV-1998.
PA (BADI) BASF AG.
Query Match 6.4%; Score 66.5; DB 2; Length 803;
Best Local Similarity 23.1%; Pred. No. 1.9e+03;
RESULT 1050
ID AAM39272 standard; protein; 803 AA.
DE Human polypeptide SEQ ID NO 2417.
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PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC. 6.4%; Score 66.5; DB 4; Length 803;
Query Match 23.1%; Pred. No. 1.9e+03;
Best Local Similarity 23.1%; Pred. No. 1.9e+03;
RESULT 1051
ID ADA45510 standard; protein; 803 AA.
DE Human Protein Q13105, SEQ ID NO 11144.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GENE-) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.4%; Score 66.5; DB 7; Length 803;
Best Local Similarity 23.1%; Pred. No. 1.9e+03;
RESULT 1052
ID ADG30638 standard; protein; 803 AA.
DE Human tubulin deacetylase-related MIZ-1 protein.
PN WO200309210-A2.
PD 04-DEC-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 6.4%; Score 66.5; DB 8; Length 803;
Best Local Similarity 23.1%; Pred. No. 1.9e+03;
RESULT 1053
ID AAM41058 standard; protein; 804 AA.
DE Human polypeptide SEQ ID NO 5989.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC. 6.4%; Score 66.5; DB 4; Length 804;
Query Match 23.1%; Pred. No. 2e+03;
Best Local Similarity 23.1%; Pred. No. 2e+03;
RESULT 1054
ID ABG01056 standard; protein; 815 AA.
DE Novel human diagnostic protein #1047.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC. 6.4%; Score 66.5; DB 4; Length 815;
Query Match 23.5%; Pred. No. 2e+03;
Best Local Similarity 23.5%; Pred. No. 2e+03;
RESULT 1055
ID ABO67256 standard; protein; 848 AA.
DE Klebsiella pneumoniae polypeptide seqid 13773.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENE-) GENOME THERAPEUTICS CORP.
Query Match 6.4%; Score 66.5; DB 7; Length 848;
Best Local Similarity 21.3%; Pred. No. 2.1e+03;
RESULT 1056
ID ADC31570 standard; protein; 893 AA.
DE Human novel polypeptide sequence, SEQ ID NO:1652.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC. 6.4%; Score 66.5; DB 7; Length 893;
Query Match 25.2%; Pred. No. 2.3e+03;
Best Local Similarity 25.2%; Pred. No. 2.3e+03;
RESULT 1057
ID ADS21876 standard; protein; 967 AA.
DE Bacterial polypeptide #10909.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.4%; Score 66.5; DB 8; Length 967;
Best Local Similarity 21.5%; Pred. No. 2.5e+03;
RESULT 1058
ID ABG07175 standard; protein; 1079 AA.
DE Novel human diagnostic protein #7166.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC. 6.4%; Score 66.5; DB 4; Length 1079;
Query Match

Best Local Similarity 20.5%; Pred. No. 2.9e+03;
RESULT 1059
ID AAW93595 standard; protein; 1445 AA.
DE O. longistaminata Xa21 gene family member D protein.
PN WO9909151-A2.
PD 25-FEB-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 6.4%; Score 66.5; DB 2; Length 1445;
Best Local Similarity 21.8%; Pred. No. 4.4e+03;
RESULT 1060
ID AD116257 standard; protein; 1453 AA.
DE Human nucleic acid-associated protein (NAAP) #42.
PN WO2003094848-A2.
PD 20-NOV-2003.
PA (INCY-) INCYTE CORP. 6.4%; Score 66.5; DB 8; Length 1453;
Query Match 23.9%; Pred. No. 4.4e+03;
Best Local Similarity 23.9%; Pred. No. 4.4e+03;
RESULT 1061
ID ABM84033 standard; protein; 1695 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4282.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP. 6.4%; Score 66.5; DB 8; Length 1695;
Query Match 20.6%; Pred. No. 5.4e+03;
Best Local Similarity 20.6%; Pred. No. 5.4e+03;
RESULT 1062
ID ADJ82955 standard; protein; 1786 AA.
DE Human latent TGF-beta-binding protein-2 mature protein.
PN WO2004005332-A2.
PD 15-JAN-2004.
PA (GENE-) GENEPROT INC. 6.4%; Score 66.5; DB 8; Length 1786;
Query Match 20.6%; Pred. No. 5.8e+03;
Best Local Similarity 20.6%; Pred. No. 5.8e+03;
RESULT 1063
ID ADN95528 standard; protein; 1820 AA.
DE Human BEC/LEC-related protein sequence SeqID451.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD. 6.4%; Score 66.5; DB 7; Length 1820;
Query Match 20.6%; Pred. No. 6e+03;
Best Local Similarity 20.6%; Pred. No. 6e+03;
RESULT 1064
ID ADA27597 standard; protein; 1821 AA.
DE Human OA4 protein SEQ ID NO:8.
PN WO2003068922-A2.
PD 21-AUG-2003.
PA (CURA-) CURAGEN CORP.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 6.4%; Score 66.5; DB 7; Length 1821;
Best Local Similarity 20.6%; Pred. No. 6e+03;
RESULT 1065
ID ADJ82954 standard; protein; 1821 AA.
DE Human latent TGF-beta-binding protein-2 precursor.
PN WO2004005332-A2.
PD 15-JAN-2004.
PA (GENE-) GENEPROT INC. 6.4%; Score 66.5; DB 8; Length 1821;
Query Match 20.6%; Pred. No. 6e+03;
Best Local Similarity 20.6%; Pred. No. 6e+03;
RESULT 1066
ID ADQ18362 standard; protein; 1821 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1181.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 6.4%; Score 66.5; DB 8; Length 1821;
Best Local Similarity 20.6%; Pred. No. 6e+03;
RESULT 1067
ID ADR51533 standard; protein; 1821 AA.
DE Human lipopolysaccharide-sensitive polypeptide #13.
PN WO2004069870-A2.
PD 19-AUG-2004.
PA (UYLE-) RIJKSUNIV LEIDEN.

Query Match 6.4%; Score 66.5; DB 8; Length 1821;
Best Local Similarity 20.6%; Pred. No. 6e+03;
RESULT 1068
ID ADR87618 standard; protein; 1821 AA.
DE Human Latent TGFbeta binding protein 2 (LTBP2), SEQ ID 22.
FN WO2004075835-A2.
PD 10-SEP-2004.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 66.5; DB 8; Length 1821;
Best Local Similarity 20.6%; Pred. No. 6e+03;
RESULT 1069
ID AAG78488 standard; protein; 1972 AA.
DE Human p53-binding protein 1.
FN WO200191629-A2.
PD 06-DEC-2001.
PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.
Query Match 6.4%; Score 66.5; DB 5; Length 1972;
Best Local Similarity 23.9%; Pred. No. 6.7e+03;
RESULT 1070
ID ADO30967 standard; protein; 1972 AA.
DE Human Polo-like kinase-related protein SeqID91.
FN WO2004046317-A2.
PD 03-JUN-2004.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
PA (YAFF/) YAFFE M B.
PA (ELIA/) ELIA A E H.
PA (RELL/) RELLOS P.
PA (CANT/) CANTLEY L C.
PA (SMER/) SMERDON S J.
PA (MANC/) MANCKE I.
Query Match 6.4%; Score 66.5; DB 8; Length 1972;
Best Local Similarity 23.9%; Pred. No. 6.7e+03;
RESULT 1071
ID ABM81612 standard; protein; 1972 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO37669, SEQ:4171.
FN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 66.5; DB 8; Length 1972;
Best Local Similarity 23.9%; Pred. No. 6.7e+03;
RESULT 1072
ID AAR24306 standard; protein; 2408 AA.
DE Translation of ORF 2 contg. E.faecium protein Vans.
FN WO9207942-A1.
PD 14-MAY-1992.
PA (INSP) INST PASTEUR.
Query Match 6.4%; Score 66.5; DB 2; Length 2408;
Best Local Similarity 21.0%; Pred. No. 8.8e+03;
RESULT 1073
ID AAU07053 standard; protein; 2956 AA.
DE Human Flamingo polypeptide.
FN WO200161003-A1.
PD 23-AUG-2001.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 6.4%; Score 66.5; DB 4; Length 2956;
Best Local Similarity 24.4%; Pred. No. 1.2e+04;
RESULT 1074
ID ABP00847 standard; protein; 65 AA.
DE Human ORFX protein sequence SEQ ID NO:1676.
FN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match 6.4%; Score 66; DB 5; Length 65;
Best Local Similarity 58.8%; Pred. No. 70;
RESULT 1075
ID AAB43279 standard; protein; 84 AA.
DE Human ORFX ORF3043 polypeptide sequence SEQ ID NO:6086.
FN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 6.4%; Score 66; DB 3; Length 84;
Best Local Similarity 48.0%; Pred. No. 1e+02;
RESULT 1076

ID ABB33674 standard; peptide; 84 AA.
DE Peptide #1180 encoded by human foetal liver single exon probe.
FN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.4%; Score 66; DB 4; Length 84;
Best Local Similarity 26.1%; Pred. No. 1e+02;
RESULT 1077
ID AM27131 standard; protein; 84 AA.
DE Peptide #1168 encoded by probe for measuring placental gene expression.
FN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.4%; Score 66; DB 4; Length 84;
Best Local Similarity 26.1%; Pred. No. 1e+02;
RESULT 1078
ID ABE28489 standard; peptide; 84 AA.
DE Peptide #1140 encoded by breast cell single exon nucleic acid probe.
FN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.4%; Score 66; DB 4; Length 84;
Best Local Similarity 26.1%; Pred. No. 1e+02;
RESULT 1079
ID AAM66848 standard; protein; 84 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 27154.
FN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.4%; Score 66; DB 4; Length 84;
Best Local Similarity 26.1%; Pred. No. 1e+02;
RESULT 1080
ID AM54443 standard; protein; 84 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 26548.
FN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.4%; Score 66; DB 4; Length 84;
Best Local Similarity 26.1%; Pred. No. 1e+02;
RESULT 1081
ID AM02433 standard; protein; 84 AA.
DE Peptide #1115 encoded by probe for measuring breast gene expression.
FN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.4%; Score 66; DB 4; Length 84;
Best Local Similarity 26.1%; Pred. No. 1e+02;
RESULT 1082
ID ABG36503 standard; peptide; 84 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 26168.
FN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.4%; Score 66; DB 5; Length 84;
Best Local Similarity 26.1%; Pred. No. 1e+02;
RESULT 1083
ID ABB58744 standard; protein; 121 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 3024.
FN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.4%; Score 66; DB 4; Length 121;
Best Local Similarity 23.9%; Pred. No. 1.6e+02;
RESULT 1084
ID ABB50199 standard; protein; 121 AA.
DE Human transcription factor TRFX-50.
FN WO200172777-A2.
PD 04-OCT-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.4%; Score 66; DB 4; Length 121;
Best Local Similarity 26.9%; Pred. No. 1.6e+02;
RESULT 1085
ID ADB75414 standard; protein; 121 AA.

DE Prostate cancer marker protein.
PN WO2003009814-A2.
PD 06-FEB-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 6.4%; Score 66; DB 7; Length 121;
Best Local Similarity 26.9%; Pred. No. 1.6e+02;
RESULT 1086
ID AD020020 standard; protein; 121 AA.
DE Human PRO polypeptide #465.
PN WO2004043361-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 66; DB 8; Length 121;
Best Local Similarity 26.9%; Pred. No. 1.6e+02;
RESULT 1087
ID ADP5188 standard; protein; 121 AA.
DE Human PRO protein sequence SEQ ID NO:1164.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 66; DB 8; Length 121;
Best Local Similarity 26.9%; Pred. No. 1.6e+02;
RESULT 1088
ID ADP24816 standard; protein; 121 AA.
DE PRO polypeptide SEQ ID NO:1994.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 66; DB 8; Length 121;
Best Local Similarity 26.9%; Pred. No. 1.6e+02;
RESULT 1089
ID ADN18561 standard; protein; 136 AA.
DE Bacterial polypeptide #1214.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.4%; Score 66; DB 8; Length 136;
Best Local Similarity 27.3%; Pred. No. 1.9e+02;
RESULT 1090
ID AAB36375 standard; protein; 194 AA.
DE Rat MLP protein sequence SEQ ID NO:11.
PN WO200066734-A1.
PD 09-NOV-2000.
PA (HARD) HARVARD COLLEGE.
Query Match 6.4%; Score 66; DB 3; Length 194;
Best Local Similarity 18.8%; Pred. No. 3.1e+02;
RESULT 1091
ID ABP58272 standard; protein; 219 AA.
DE Humanised 3D6 antibody light chain.
PN WO200288306-A2.
PD 07-NOV-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 6.4%; Score 66; DB 6; Length 219;
Best Local Similarity 23.3%; Pred. No. 3.7e+02;
RESULT 1092
ID ABG22964 standard; protein; 221 AA.
DE Novel human diagnostic protein #22955.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 66; DB 4; Length 221;
Best Local Similarity 25.2%; Pred. No. 3.8e+02;
RESULT 1093
ID ABG03524 standard; protein; 221 AA.
DE Novel human diagnostic protein #3515.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 66; DB 4; Length 221;
Best Local Similarity 25.2%; Pred. No. 3.8e+02;
RESULT 1094
ID ABG11678 standard; protein; 221 AA.
DE Novel human diagnostic protein #11669.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 66; DB 4; Length 221;
Best Local Similarity 25.2%; Pred. No. 3.8e+02;
RESULT 1095
ID ABP58274 standard; protein; 239 AA.
DE Humanised 3D6 antibody light chain.
PN WO200288306-A2.
PD 07-NOV-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 6.4%; Score 66; DB 6; Length 239;
Best Local Similarity 23.3%; Pred. No. 4.2e+02;
RESULT 1096
ID AAB56601 standard; protein; 249 AA.
DE Human prostate cancer antigen protein sequence SEQ ID NO:1179.
PN WO200055174-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.4%; Score 66; DB 3; Length 249;
Best Local Similarity 25.4%; Pred. No. 4.4e+02;
RESULT 1097
ID AAG07186 standard; protein; 256 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4243.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 66; DB 3; Length 256;
Best Local Similarity 22.0%; Pred. No. 4.6e+02;
RESULT 1098
ID AAU16053 standard; protein; 265 AA.
DE Human novel secreted protein, Seq ID 1006.
PN WO200155322-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.4%; Score 66; DB 4; Length 265;
Best Local Similarity 22.7%; Pred. No. 4.8e+02;
RESULT 1099
ID ABU55122 standard; protein; 265 AA.
DE Human novel polypeptide #209.
PN US2002132753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 6.4%; Score 66; DB 6; Length 265;
Best Local Similarity 22.7%; Pred. No. 4.8e+02;
RESULT 1100
ID ADF59371 standard; protein; 280 AA.
DE Human polypeptide sequence SEQ ID NO:1779.
PN WO2003080795-A2.
PD 02-OCT-2003.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 66; DB 7; Length 280;
Best Local Similarity 19.4%; Pred. No. 5.2e+02;
RESULT 1101
ID AAG07185 standard; protein; 325 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4242.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 66; DB 3; Length 325;
Best Local Similarity 22.0%; Pred. No. 6.4e+02;
RESULT 1102
ID ABM68479 standard; protein; 360 AA.
DE Photorhabdus luminescens protein sequence #1576.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.

Query Match 6.4%; Score 66; DB 6; Length 360;
Best Local Similarity 20.5%; Pred. No. 7.3e+02;
RESULT 1103
ID ADR08292 standard; protein; 375 AA.
DE Novel protein (useful for identifying genetic disorders) #447.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 66; DB 7; Length 375;
Best Local Similarity 61.9%; Pred. No. 7.7e+02;
RESULT 1104
ID AAR29952 standard; protein; 380 AA.
DE Bacillus amyloliquefaciens subtilisin-like protein #19.
PN WO200277289-A1.
PD 03-OCT-2002.
PA (HERC) HERCULES INC.
Query Match 6.4%; Score 66; DB 6; Length 380;
Best Local Similarity 20.5%; Pred. No. 7.9e+02;
RESULT 1105
ID ABB71820 standard; protein; 402 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 42252.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.4%; Score 66; DB 4; Length 402;
Best Local Similarity 20.7%; Pred. No. 8.5e+02;
RESULT 1106
ID ADP04777 standard; protein; 453 AA.
DE Sea squirt protein with tissue specific expression in development Seq372.
PN JP2004057129-A.
PD 26-FEB-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 6.4%; Score 66; DB 8; Length 453;
Best Local Similarity 24.6%; Pred. No. 1e+03;
RESULT 1107
ID ADR0315 standard; protein; 460 AA.
DE Clostridium josui cellulose degrading cellulase B protein.
PN JP2004261144-A.
PD 24-SEP-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
PA (MIED-) UNIV MIE.
Query Match 6.4%; Score 66; DB 8; Length 460;
Best Local Similarity 24.2%; Pred. No. 1e+03;
RESULT 1108
ID ABG21358 standard; protein; 480 AA.
DE Novel human diagnostic protein #21349.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 66; DB 4; Length 480;
Best Local Similarity 21.6%; Pred. No. 1.1e+03;
RESULT 1109
ID ABB50229 standard; protein; 482 AA.
DE Human transcription factor TRFX-80.
PN WO200172777-A2.
PD 04-OCT-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.4%; Score 66; DB 4; Length 482;
Best Local Similarity 22.6%; Pred. No. 1.1e+03;
RESULT 1110
ID ADF44681 standard; protein; 514 AA.
DE Human NOV4a protein SEQ ID NO:28.
PN WO2003066881-A2.
PD 14-AUG-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.4%; Score 66; DB 7; Length 514;
Best Local Similarity 16.7%; Pred. No. 1.2e+03;
RESULT 1111
ID AAB46748 standard; protein; 522 AA.
DE R. marinus bacteriophage RM387 ORF632e protein.
PN WO200075335-A2.
PD 14-DEC-2000.
PA (DECO-) DECODE GENETICS EHF.

Query Match 6.4%; Score 66; DB 4; Length 522;
Best Local Similarity 29.0%; Pred. No. 1.2e+03;
RESULT 1112
ID ABG21352 standard; protein; 549 AA.
DE Novel human diagnostic protein #21343.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 66; DB 4; Length 549;
Best Local Similarity 21.6%; Pred. No. 1.3e+03;
RESULT 1113
ID ABB61988 standard; protein; 553 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 12756.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.4%; Score 66; DB 4; Length 553;
Best Local Similarity 29.1%; Pred. No. 1.3e+03;
RESULT 1114
ID AUN99733 standard; protein; 592 AA.
DE Novel human protein sequence #549.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 6.4%; Score 66; DB 8; Length 592;
Best Local Similarity 22.6%; Pred. No. 1.4e+03;
RESULT 1115
ID AAB92780 standard; protein; 625 AA.
DE Human protein sequence SEQ ID NO:11266.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 6.4%; Score 66; DB 4; Length 625;
Best Local Similarity 24.6%; Pred. No. 1.6e+03;
RESULT 1116
ID ABB82300 standard; protein; 634 AA.
DE CD19:zeta chimeric immunoreceptor.
PN WO200277029-A2.
PD 03-OCT-2002.
PA (CITY) CITY OF HOPE.
Query Match 6.4%; Score 66; DB 6; Length 634;
Best Local Similarity 21.3%; Pred. No. 1.6e+03;
RESULT 1117
ID AAM40146 standard; protein; 636 AA.
DE Human polypeptide SEQ ID NO 3291.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 66; DB 4; Length 636;
Best Local Similarity 24.7%; Pred. No. 1.6e+03;
RESULT 1118
ID ABB77378 standard; protein; 669 AA.
DE Rice acyl CoA oxidase homologue SEQ ID NO 18.
PN US636840-B1.
PD 09-APR-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 6.4%; Score 66; DB 5; Length 669;
Best Local Similarity 27.1%; Pred. No. 1.7e+03;
RESULT 1119
ID AAY96449 standard; protein; 673 AA.
DE Forkhead transcription factor FKHL1.
PN WO200031291-A1.
PD 02-JUN-2000.
PA (PHAA) PHARMACIA & UPJOHN AB.
Query Match 6.4%; Score 66; DB 3; Length 673;
Best Local Similarity 23.5%; Pred. No. 1.7e+03;
RESULT 1120
ID ADO22520 standard; protein; 673 AA.
DE Biochemical pathway-related human FKHL1 protein SeqID6.
PN WO200404218-A2.
PD 27-MAY-2004.
PA (REGC) UNIV CALIFORNIA.
PA (CELL-) CELL SIGNALING TECHNOLOGY INC.

Query Match 6.4%; Score 66; DB 8; Length 673;
Best Local Similarity 23.5%; Pred. No. 1.7e+03;
RESULT 1121
ID ADP23662 standard; protein; 673 AA.
DE PRO polypeptide SEQ ID NO:840.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 66; DB 8; Length 673;
Best Local Similarity 23.5%; Pred. No. 1.7e+03;
RESULT 1122
ID ABG28399 standard; protein; 693 AA.
DE Novel human diagnostic protein #28390.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 66; DB 4; Length 693;
Best Local Similarity 26.2%; Pred. No. 1.8e+03;
RESULT 1123
ID AAY08471 standard; protein; 699 AA.
DE F. balustinum CP70 protein.
PN WO9925848-A1.
PD 27-MAY-1999.
PA (PROC) PROCTER & GAMBLE CO.
Query Match 6.4%; Score 66; DB 2; Length 699;
Best Local Similarity 23.7%; Pred. No. 1.8e+03;
RESULT 1124
ID ABU27768 standard; protein; 701 AA.
DE Protein encoded by Prokaryotic essential gene #13295.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.4%; Score 66; DB 6; Length 701;
Best Local Similarity 22.9%; Pred. No. 1.8e+03;
RESULT 1125
ID AAY37234 standard; protein; 708 AA.
DE Chlamydia trachomatis cellular envelope protein.
PN WO9928475-A2.
PD 10-JUN-1999.
PA (GEST) GENSET.
Query Match 6.4%; Score 66; DB 2; Length 708;
Best Local Similarity 21.9%; Pred. No. 1.8e+03;
RESULT 1126
ID AAM30617 standard; protein; 751 AA.
DE Human semaphorin E protein from clone BR5334.
PN WO9853065-A1.
PD 26-NOV-1998.
PA (GEMY) GENETICS INST INC.
Query Match 6.4%; Score 66; DB 2; Length 751;
Best Local Similarity 16.7%; Pred. No. 2e+03;
RESULT 1127
ID AAB28379 standard; protein; 751 AA.
DE Clone BR533 4.
PN WO200063692-A1.
PD 26-OCT-2000.
PA (GEMY) GENETICS INST INC.
Query Match 6.4%; Score 66; DB 3; Length 751;
Best Local Similarity 16.7%; Pred. No. 2e+03;
RESULT 1128
ID AAG62728 standard; peptide; 751 AA.
DE Amino acid sequence of human semaphorin Sema3C.
PN WO200138491-A2.
PD 31-MAY-2001.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 6.4%; Score 66; DB 4; Length 751;
Best Local Similarity 16.7%; Pred. No. 2e+03;
RESULT 1129
ID ABP68623 standard; protein; 751 AA.
DE Human pancreatic cancer expressed protein SEQ ID NO 172.
PN WO200260317-A2.
PD 08-AUG-2002.
PA (CORI-) CORIXA CORP.
Query Match 6.4%; Score 66; DB 5; Length 751;
Best Local Similarity 16.7%; Pred. No. 2e+03;
RESULT 1130
ID ABU89764 standard; protein; 751 AA.
DE Protein differentially expressed in cardiovascular disease #58.
PN WO2003031650-A2.
PD 17-APR-2003.
PA (FARB) BAYER AG.
Query Match 6.4%; Score 66; DB 6; Length 751;
Best Local Similarity 16.7%; Pred. No. 2e+03;
RESULT 1131
ID ADB75535 standard; protein; 751 AA.
DE Prostate cancer marker protein.
PN WO2003009814-A2.
PD 06-FEB-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 6.4%; Score 66; DB 7; Length 751;
Best Local Similarity 16.7%; Pred. No. 2e+03;
RESULT 1132
ID ADC38856 standard; protein; 751 AA.
DE Human secreted protein #100.
PN US2002193567-A1.
PD 19-DEC-2002.
PA (GEMY) GENETICS INST INC.
Query Match 6.4%; Score 66; DB 7; Length 751;
Best Local Similarity 16.7%; Pred. No. 2e+03;
RESULT 1133
ID ADD08938 standard; protein; 751 AA.
DE Human semaphorin 3C protein SEQ ID NO:14.
PN WO2003029814-A2.
PD 10-APR-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 6.4%; Score 66; DB 7; Length 751;
Best Local Similarity 16.7%; Pred. No. 2e+03;
RESULT 1134
ID ADQ19446 standard; protein; 751 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2265.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 6.4%; Score 66; DB 8; Length 751;
Best Local Similarity 16.7%; Pred. No. 2e+03;
RESULT 1135
ID ADP23608 standard; protein; 751 AA.
DE PRO polypeptide SEQ ID NO:786.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 66; DB 8; Length 751;
Best Local Similarity 16.7%; Pred. No. 2e+03;
RESULT 1136
ID ADR39825 standard; protein; 783 AA.
DE Human NRC interacting factor-2 (NIF-2) seqid 6.
PN US2004175720-A1.
PD 09-SEP-2004.
PA (MAHA/) MAHAJAN M A.
PA (SAMU/) SAMUELS H H.
Query Match 6.4%; Score 66; DB 8; Length 783;
Best Local Similarity 22.7%; Pred. No. 2.1e+03;
RESULT 1137
ID AAY34870 standard; protein; 789 AA.
DE C. pneumoniae protein involved in metabolism of nucleic acids.
PN WO9927105-A2.
PD 03-JUN-1999.
PA (GEST) GENSET.
Query Match 6.4%; Score 66; DB 2; Length 789;
Best Local Similarity 27.2%; Pred. No. 2.1e+03;
RESULT 1138
ID ABB94258 standard; protein; 805 AA.
DE Chlamydia pneumoniae protein sequence SEQ ID NO:386.
PN WO200208267-A2.
PD 31-JAN-2002.
PA (CORI-) CORIXA CORP.

Query Match 6.4%; Score 66; DB 5; Length 805;
Best Local Similarity 27.2%; Pred. No. 2.2e+03;
RESULT 1139
ID ABU26908 standard; protein; 805 AA.
DE Protein encoded by Prokaryotic essential gene #12435.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.4%; Score 66; DB 6; Length 805;
Best Local Similarity 27.2%; Pred. No. 2.2e+03;
RESULT 1140
ID ADL96642 standard; protein; 835 AA.
DE M. paratuberculosis polypeptide #10.
PN US2003175725-A1.
PD 18-SEP-2003.
PA (KAPU/) KAPUR V.
PA (BANN/) BANNANTINE J P.
Query Match 6.4%; Score 66; DB 7; Length 835;
Best Local Similarity 24.2%; Pred. No. 2.3e+03;
RESULT 1141
ID ADL16585 standard; protein; 849 AA.
DE Human 282PIG3 polypeptide #35.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 849;
Best Local Similarity 21.6%; Pred. No. 2.4e+03;
RESULT 1142
ID ADL16586 standard; protein; 851 AA.
DE Human 282PIG3 polypeptide #36.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 851;
Best Local Similarity 21.6%; Pred. No. 2.4e+03;
RESULT 1143
ID ABA6727 standard; protein; 871 AA.
DE R. marinus bacteriophage RM378 DNA polymerase protein SEQ ID NO 36.
PN WO200075335-A2.
PD 14-DEC-2000.
PA (DECO-) DECODE GENETICS EHF.
Query Match 6.4%; Score 66; DB 4; Length 871;
Best Local Similarity 29.0%; Pred. No. 2.5e+03;
RESULT 1144
ID ADL16446 standard; protein; 893 AA.
DE Human 282PIG3 polypeptide #12.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 893;
Best Local Similarity 21.6%; Pred. No. 2.5e+03;
RESULT 1145
ID ADL16584 standard; protein; 893 AA.
DE Human 282PIG3 polypeptide #34.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 893;
Best Local Similarity 21.6%; Pred. No. 2.5e+03;
RESULT 1146
ID ADL16625 standard; protein; 893 AA.
DE Human 282PIG3 polypeptide #57.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 893;
Best Local Similarity 21.6%; Pred. No. 2.5e+03;
RESULT 1147
ID ADL16431 standard; protein; 893 AA.
DE Human 282PIG3 polypeptide #3.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.

Query Match 6.4%; Score 66; DB 8; Length 893;
Best Local Similarity 21.6%; Pred. No. 2.5e+03;
RESULT 1148
ID AAB93294 standard; protein; 964 AA.
DE Human protein sequence SEQ ID NO:12355.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 6.4%; Score 66; DB 4; Length 964;
Best Local Similarity 24.6%; Pred. No. 2.8e+03;
RESULT 1149
ID ABG24301 standard; protein; 975 AA.
DE Novel human diagnostic protein #24292.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 66; DB 4; Length 975;
Best Local Similarity 25.4%; Pred. No. 2.9e+03;
RESULT 1150
ID ABG25520 standard; protein; 994 AA.
DE Novel human diagnostic protein #25511.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 66; DB 4; Length 994;
Best Local Similarity 25.4%; Pred. No. 2.9e+03;
RESULT 1151
ID AAB92858 standard; protein; 1045 AA.
DE Human protein sequence SEQ ID NO:11431.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 6.4%; Score 66; DB 4; Length 1045;
Best Local Similarity 24.6%; Pred. No. 3.1e+03;
RESULT 1152
ID ADR08740 standard; protein; 1113 AA.
DE Human protein useful for treating neurological disease Seq 2246.
PN EP1474713-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.4%; Score 66; DB 8; Length 1113;
Best Local Similarity 21.6%; Pred. No. 3.4e+03;
RESULT 1153
ID ADL16626 standard; protein; 1117 AA.
DE Human 282PIG3 polypeptide #58.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 1117;
Best Local Similarity 21.6%; Pred. No. 3.5e+03;
RESULT 1154
ID ADL16590 standard; protein; 1117 AA.
DE Human 282PIG3 polypeptide #37.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 1117;
Best Local Similarity 21.6%; Pred. No. 3.5e+03;
RESULT 1155
ID ADL16447 standard; protein; 1117 AA.
DE Human 282PIG3 polypeptide #13.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 1117;
Best Local Similarity 21.6%; Pred. No. 3.5e+03;
RESULT 1156
ID ADL16433 standard; protein; 1117 AA.
DE Human 282PIG3 polypeptide #4.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 1117;
Best Local Similarity 21.6%; Pred. No. 3.5e+03;
RESULT 1157
ID ADL16433 standard; protein; 1117 AA.
DE Human 282PIG3 polypeptide #4.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 1117;


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Best Local Similarity 21.6%; Pred. No. 3.5e+03;
RESULT 1157
ID ADL16592 standard; protein; 1117 AA.
DE Human 282PIG3 polypeptide #39.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 1117;
Best Local Similarity 21.6%; Pred. No. 3.5e+03;
RESULT 1158
ID ADL16578 standard; protein; 1171 AA.
DE Human 282PIG3 polypeptide #31.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 1171;
Best Local Similarity 21.6%; Pred. No. 3.7e+03;
RESULT 1159
ID ADL16624 standard; protein; 1171 AA.
DE Human 282PIG3 polypeptide #56.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 1171;
Best Local Similarity 21.6%; Pred. No. 3.7e+03;
RESULT 1160
ID ADL16580 standard; protein; 1171 AA.
DE Human 282PIG3 polypeptide #33.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 1171;
Best Local Similarity 21.6%; Pred. No. 3.7e+03;
RESULT 1161
ID ADL16429 standard; protein; 1171 AA.
DE Human 282PIG3 polypeptide #2.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 1171;
Best Local Similarity 21.6%; Pred. No. 3.7e+03;
RESULT 1162
ID ADL16445 standard; protein; 1171 AA.
DE Human 282PIG3 polypeptide #11.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 1171;
Best Local Similarity 21.6%; Pred. No. 3.7e+03;
RESULT 1163
ID ABM83685 standard; protein; 1171 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3934.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.4%; Score 66; DB 8; Length 1171;
Best Local Similarity 21.6%; Pred. No. 3.7e+03;
RESULT 1164
ID ADL16604 standard; protein; 1183 AA.
DE Human 282PIG3 polypeptide #45.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 1183;
Best Local Similarity 21.6%; Pred. No. 3.7e+03;
RESULT 1165
ID ADL16628 standard; protein; 1183 AA.
DE Human 282PIG3 polypeptide #60.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 1183;
Best Local Similarity 21.6%; Pred. No. 3.7e+03;
RESULT 1166
ID ADL16449 standard; protein; 1183 AA.
DE Human 282PIG3 polypeptide #15.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 1183;
Best Local Similarity 21.6%; Pred. No. 3.7e+03;
RESULT 1167
ID ADL16602 standard; protein; 1183 AA.
DE Human 282PIG3 polypeptide #43.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 1183;
Best Local Similarity 21.6%; Pred. No. 3.7e+03;
RESULT 1168
ID ADL16437 standard; protein; 1183 AA.
DE Human 282PIG3 polypeptide #6.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 1183;
Best Local Similarity 21.6%; Pred. No. 3.7e+03;
RESULT 1169
ID AD863195 standard; protein; 1186 AA.
DE Rat Protein AAB58646, SEQ ID NO 9132.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.4%; Score 66; DB 7; Length 1186;
Best Local Similarity 22.2%; Pred. No. 3.7e+03;
RESULT 1170
ID AD863203 standard; protein; 1186 AA.
DE Rat Protein AAB58646, SEQ ID NO 9140.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.4%; Score 66; DB 7; Length 1186;
Best Local Similarity 22.2%; Pred. No. 3.7e+03;
RESULT 1171
ID AD863207 standard; protein; 1186 AA.
DE Rat Protein AAB58646, SEQ ID NO 9144.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.4%; Score 66; DB 7; Length 1186;
Best Local Similarity 22.2%; Pred. No. 3.7e+03;
RESULT 1172
ID AD863199 standard; protein; 1186 AA.
DE Rat Protein AAB58646, SEQ ID NO 9136.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.4%; Score 66; DB 7; Length 1186;
Best Local Similarity 22.2%; Pred. No. 3.7e+03;
RESULT 1173
ID ADL16630 standard; protein; 1195 AA.
DE Human 282PIG3 polypeptide #62.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 1195;
Best Local Similarity 21.6%; Pred. No. 3.8e+03;
RESULT 1174
ID ADL16451 standard; protein; 1195 AA.
DE Human 282PIG3 polypeptide #17.
PN WO2004016734-A2.
PD 26-FEB-2004.
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PA (AGEN-) AGENSYS INC. 6.4%; Score 66; DB 8; Length 1195;
Query Match Best Local Similarity 21.6%; Pred. No. 3.8e+03;
RESULT 1175
ID ADL16441 standard; protein; 1195 AA.
DE Human 282PIG3 polypeptide #8.
FN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC. 6.4%; Score 66; DB 8; Length 1195;
Query Match Best Local Similarity 21.6%; Pred. No. 3.8e+03;
RESULT 1176
ID ADL16616 standard; protein; 1195 AA.
DE Human 282PIG3 polypeptide #51.
FN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC. 6.4%; Score 66; DB 8; Length 1195;
Query Match Best Local Similarity 21.6%; Pred. No. 3.8e+03;
RESULT 1177
ID ADL16614 standard; protein; 1195 AA.
DE Human 282PIG3 polypeptide #49.
FN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC. 6.4%; Score 66; DB 8; Length 1195;
Query Match Best Local Similarity 21.6%; Pred. No. 3.8e+03;
RESULT 1178
ID ADL16448 standard; protein; 1208 AA.
DE Human 282PIG3 polypeptide #14.
FN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC. 6.4%; Score 66; DB 8; Length 1208;
Query Match Best Local Similarity 21.6%; Pred. No. 3.8e+03;
RESULT 1179
ID ADL16596 standard; protein; 1208 AA.
DE Human 282PIG3 polypeptide #40.
FN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC. 6.4%; Score 66; DB 8; Length 1208;
Query Match Best Local Similarity 21.6%; Pred. No. 3.8e+03;
RESULT 1180
ID ADL16435 standard; protein; 1208 AA.
DE Human 282PIG3 polypeptide #5.
FN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC. 6.4%; Score 66; DB 8; Length 1208;
Query Match Best Local Similarity 21.6%; Pred. No. 3.8e+03;
RESULT 1181
ID ADL16627 standard; protein; 1208 AA.
DE Human 282PIG3 polypeptide #59.
FN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC. 6.4%; Score 66; DB 8; Length 1208;
Query Match Best Local Similarity 21.6%; Pred. No. 3.8e+03;
RESULT 1182
ID ADL16598 standard; protein; 1208 AA.
DE Human 282PIG3 polypeptide #42.
FN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC. 6.4%; Score 66; DB 8; Length 1208;
Query Match Best Local Similarity 21.6%; Pred. No. 3.8e+03;
RESULT 1183
ID ADE55236 standard; protein; 1224 AA.
DE Human Protein AAB60937, SEQ ID NO 1049.
FN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG. 6.4%; Score 66; DB 7; Length 1224;
Query Match Best Local Similarity 21.6%; Pred. No. 3.9e+03;
RESULT 1184
ID ADJ69602 standard; protein; 1224 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1408.
FN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR. 6.4%; Score 66; DB 7; Length 1224;
PA (BUCK-) BUCK INST AGE RES. 6.4%; Score 66; DB 7; Length 1224;
Query Match Best Local Similarity 21.6%; Pred. No. 3.9e+03;
RESULT 1185
ID ADL15032 standard; protein; 1224 AA.
DE Human neural cell adhesion molecule protein for cancer treatment.
FN WO2003068268-A2.
PD 21-AUG-2003.
PA (BIOI-) BIOINVENT INT AB. 6.4%; Score 66; DB 7; Length 1224;
Query Match Best Local Similarity 21.6%; Pred. No. 3.9e+03;
RESULT 1186
ID ADJ75519 standard; protein; 1224 AA.
DE Marker Gene related amino acid sequence SEQ ID NO:771.
FN EPI394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC. 6.4%; Score 66; DB 8; Length 1224;
Query Match Best Local Similarity 21.6%; Pred. No. 3.9e+03;
RESULT 1187
ID ADL16443 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #9.
FN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC. 6.4%; Score 66; DB 8; Length 1224;
Query Match Best Local Similarity 21.6%; Pred. No. 3.9e+03;
RESULT 1188
ID ADL16597 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #41.
FN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC. 6.4%; Score 66; DB 8; Length 1224;
Query Match Best Local Similarity 21.6%; Pred. No. 3.9e+03;
RESULT 1189
ID ADL16621 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #53.
FN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC. 6.4%; Score 66; DB 8; Length 1224;
Query Match Best Local Similarity 21.6%; Pred. No. 3.9e+03;
RESULT 1190
ID ADL16452 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #18.
FN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC. 6.4%; Score 66; DB 8; Length 1224;
Query Match Best Local Similarity 21.6%; Pred. No. 3.9e+03;
RESULT 1191
ID ADL16454 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #20.
FN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC. 6.4%; Score 66; DB 8; Length 1224;
Query Match Best Local Similarity 21.6%; Pred. No. 3.9e+03;
RESULT 1192
ID ADL16579 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #32.
FN WO2004016734-A2.
PD 26-FEB-2004.

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PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 1224;
Best Local Similarity 21.6%; Pred. No. 3.9e+03;
RESULT 1193
ID ADL16427 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #1.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 1224;
Best Local Similarity 21.6%; Pred. No. 3.9e+03;
RESULT 1194
ID ADL16455 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #21.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 1224;
Best Local Similarity 21.6%; Pred. No. 3.9e+03;
RESULT 1195
ID ADL16457 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #23.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 1224;
Best Local Similarity 21.6%; Pred. No. 3.9e+03;
RESULT 1196
ID ADL16591 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #38.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 1224;
Best Local Similarity 21.6%; Pred. No. 3.9e+03;
RESULT 1197
ID ADL16620 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #52.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 1224;
Best Local Similarity 21.6%; Pred. No. 3.9e+03;
RESULT 1198
ID ADL16456 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #22.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 1224;
Best Local Similarity 21.6%; Pred. No. 3.9e+03;
RESULT 1199
ID ADL16615 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #50.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 1224;
Best Local Similarity 21.6%; Pred. No. 3.9e+03;
RESULT 1200
ID ADL16622 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #54.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 1224;
Best Local Similarity 21.6%; Pred. No. 3.9e+03;
RESULT 1201
ID ADL16444 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #10.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 1224;
Best Local Similarity 21.6%; Pred. No. 3.9e+03;
RESULT 1202
ID ADL16458 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #24.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 1224;
Best Local Similarity 21.6%; Pred. No. 3.9e+03;
RESULT 1203
ID ADL16550 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #27.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 1224;
Best Local Similarity 21.6%; Pred. No. 3.9e+03;
RESULT 1204
ID ADL16459 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #25.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 1224;
Best Local Similarity 21.6%; Pred. No. 3.9e+03;
RESULT 1205
ID ADL16603 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #44.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 1224;
Best Local Similarity 21.6%; Pred. No. 3.9e+03;
RESULT 1206
ID ADL16453 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #19.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 1224;
Best Local Similarity 21.6%; Pred. No. 3.9e+03;
RESULT 1207
ID ADL16632 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #63.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 1224;
Best Local Similarity 21.6%; Pred. No. 3.9e+03;
RESULT 1208
ID ADL16609 standard; protein; 1224 AA.
DE Human 282PIG3 polypeptide #47.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 1224;
Best Local Similarity 21.6%; Pred. No. 3.9e+03;
RESULT 1209
ID ADN04062 standard; protein; 1224 AA.
DE Antipsoriatic protein sequence #226.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GENTECH) INC.
Query Match 6.4%; Score 66; DB 8; Length 1224;
Best Local Similarity 21.6%; Pred. No. 3.9e+03;
RESULT 1210
ID ADQ19766 standard; protein; 1224 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2585.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 6.4%; Score 66; DB 8; Length 1224;
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Best Local Similarity 21.6%; Pred. No. 3.9e+03;
RESULT 1211
ID ADRI4776 standard; protein; 1224 AA.
DE Amino acid sequence of human MAPCAX orthologue #8.
PN WO2004066948-A2.
PD 12-AUG-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 6.4%; Score 66; DB 8; Length 1224;
Best Local Similarity 21.6%; Pred. No. 3.9e+03;
RESULT 1212
ID ABP68968 standard; protein; 1234 AA.
DE Human polypeptide SEQ ID NO 1015.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 66; DB 5; Length 1234;
Best Local Similarity 22.7%; Pred. No. 4e+03;
RESULT 1213
ID ADLI6629 standard; protein; 1236 AA.
DE Human 282PIG3 polypeptide #61.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 1236;
Best Local Similarity 21.6%; Pred. No. 4e+03;
RESULT 1214
ID ADLI6439 standard; protein; 1236 AA.
DE Human 282PIG3 polypeptide #7.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 1236;
Best Local Similarity 21.6%; Pred. No. 4e+03;
RESULT 1215
ID ADLI6450 standard; protein; 1236 AA.
DE Human 282PIG3 polypeptide #16.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 1236;
Best Local Similarity 21.6%; Pred. No. 4e+03;
RESULT 1216
ID ADLI6608 standard; protein; 1236 AA.
DE Human 282PIG3 polypeptide #46.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 1236;
Best Local Similarity 21.6%; Pred. No. 4e+03;
RESULT 1217
ID ADLI6610 standard; protein; 1236 AA.
DE Human 282PIG3 polypeptide #48.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 66; DB 8; Length 1236;
Best Local Similarity 21.6%; Pred. No. 4e+03;
RESULT 1218
ID ABM85838 standard; protein; 1243 AA.
DE Mouse protein sequence mCPI3907.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 6.4%; Score 66; DB 7; Length 1243;
Best Local Similarity 18.7%; Pred. No. 4e+03;
RESULT 1219
ID ABG28292 standard; protein; 1337 AA.
DE Novel human diagnostic protein #28283.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 66; DB 4; Length 1337;
Best Local Similarity 25.8%; Pred. No. 4.4e+03;

RESULT 1220
ID ADR39822 standard; protein; 1342 AA.
DE Human NRC interacting factor-1 (NIF-1) seqid 3.
PN US2004175720-A1.
PD 09-SEP-2004.
PA (MAHA/) MAHAJAN M A.
PA (SAMU/) SAMUELS H H.
Query Match 6.4%; Score 66; DB 8; Length 1342;
Best Local Similarity 22.7%; Pred. No. 4.4e+03;
RESULT 1221
ID ADR39821 standard; protein; 1357 AA.
DE Human NRC interacting factor-1 (NIF-1) seqid 2.
PN US2004175720-A1.
PD 09-SEP-2004.
PA (MAHA/) MAHAJAN M A.
PA (SAMU/) SAMUELS H H.
Query Match 6.4%; Score 66; DB 8; Length 1357;
Best Local Similarity 22.7%; Pred. No. 4.5e+03;
RESULT 1222
ID ADP30025 standard; protein; 1560 AA.
DE Human secreted protein SEQ ID #792.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 6.4%; Score 66; DB 8; Length 1560;
Best Local Similarity 22.7%; Pred. No. 5.5e+03;
RESULT 1223
ID ADP30024 standard; protein; 1615 AA.
DE Human secreted protein SEQ ID #791.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 6.4%; Score 66; DB 8; Length 1615;
Best Local Similarity 22.7%; Pred. No. 5.7e+03;
RESULT 1224
ID ADQ21674 standard; protein; 1769 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 4494.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 6.4%; Score 66; DB 8; Length 1769;
Best Local Similarity 24.6%; Pred. No. 6.5e+03;
RESULT 1225
ID ADI16955 standard; protein; 2346 AA.
DE Murine NOVX protein homologue SeqID 491.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 6.4%; Score 66; DB 5; Length 2346;
Best Local Similarity 24.6%; Pred. No. 9.5e+03;
RESULT 1226
ID ABP53589 standard; protein; 2613 AA.
DE Human NOV15d protein SEQ ID NO:42.
PN WO200262999-A2.
PD 15-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 6.4%; Score 66; DB 5; Length 2613;
Best Local Similarity 24.6%; Pred. No. 1.1e+04;
RESULT 1227
ID ADH41977 standard; protein; 2613 AA.
DE Novel human protein NOV40w.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.4%; Score 66; DB 8; Length 2613;
Best Local Similarity 24.6%; Pred. No. 1.1e+04;
RESULT 1228
ID ABP53588 standard; protein; 2628 AA.
DE Human NOV15c protein SEQ ID NO:40.
PN WO200262999-A2.
PD 15-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 6.4%; Score 66; DB 5; Length 2628;

Best Local Similarity 24.6%; Pred. No. 1.1e+04;
RESULT 1229
ID ADH41949 standard; protein; 2628 AA.
DE Novel human protein NOV401.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.4%; Score 66; DB 8; Length 2628;
Best Local Similarity 24.6%; Pred. No. 1.1e+04;
RESULT 1230
ID ABP53587 standard; protein; 2721 AA.
DE Human NOV15b protein SEQ ID NO:38.
PN WO200262999-A2.
PD 15-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 6.4%; Score 66; DB 5; Length 2721;
Best Local Similarity 24.6%; Pred. No. 1.2e+04;
RESULT 1231
ID ADH41969 standard; protein; 2721 AA.
DE Novel human protein NOV408.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.4%; Score 66; DB 8; Length 2721;
Best Local Similarity 24.6%; Pred. No. 1.2e+04;
RESULT 1232
ID ABP53586 standard; protein; 2725 AA.
DE Human NOV15a protein SEQ ID NO:36.
PN WO200262999-A2.
PD 15-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 6.4%; Score 66; DB 5; Length 2725;
Best Local Similarity 24.6%; Pred. No. 1.2e+04;
RESULT 1233
ID ADH41995 standard; protein; 2725 AA.
DE Novel human protein NOV40f #2.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.4%; Score 66; DB 8; Length 2725;
Best Local Similarity 24.6%; Pred. No. 1.2e+04;
RESULT 1234
ID ADH41991 standard; protein; 2725 AA.
DE Novel human protein NOV40d #2.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.4%; Score 66; DB 8; Length 2725;
Best Local Similarity 24.6%; Pred. No. 1.2e+04;
RESULT 1235
ID ADH41933 standard; protein; 2725 AA.
DE Novel human protein NOV40a.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.4%; Score 66; DB 8; Length 2725;
Best Local Similarity 24.6%; Pred. No. 1.2e+04;
RESULT 1236
ID ADH41997 standard; protein; 2725 AA.
DE Novel human protein NOV40g #2.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.4%; Score 66; DB 8; Length 2725;
Best Local Similarity 24.6%; Pred. No. 1.2e+04;
RESULT 1237
ID ADH41993 standard; protein; 2725 AA.
DE Novel human protein NOV40e #2.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.4%; Score 66; DB 8; Length 2725;
Best Local Similarity 24.6%; Pred. No. 1.2e+04;

RESULT 1238
ID ADH41999 standard; protein; 2725 AA.
DE Novel human protein NOV40h #2.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.4%; Score 66; DB 8; Length 2725;
Best Local Similarity 24.6%; Pred. No. 1.2e+04;
RESULT 1239
ID ADH41973 standard; protein; 2725 AA.
DE Novel human protein NOV40u.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.4%; Score 66; DB 8; Length 2725;
Best Local Similarity 24.6%; Pred. No. 1.2e+04;
RESULT 1240
ID ABB58102 standard; protein; 3005 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 1098.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.4%; Score 66; DB 4; Length 3005;
Best Local Similarity 21.3%; Pred. No. 1.3e+04;
RESULT 1241
ID AAB19796 standard; protein; 3084 AA.
DE Mouse laminin 2 mature alpha-2 chain.
PN WO200066730-A2.
PD 09-NOV-2000.
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
Query Match 6.4%; Score 66; DB 3; Length 3084;
Best Local Similarity 26.5%; Pred. No. 1.4e+04;
RESULT 1242
ID ADS17493 standard; protein; 3084 AA.
DE Amino acid sequence of murine laminin-2 alpha chain.
PN WO2004079007-A2.
PD 16-SEP-2004.
PA (NNAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
Query Match 6.4%; Score 66; DB 8; Length 3084;
Best Local Similarity 26.5%; Pred. No. 1.4e+04;
RESULT 1243
ID ADR97662 standard; protein; 3084 AA.
DE Murine laminin alpha chain protein, an actin acting substance SeqID 6.
PN WO2004079332-A2.
PD 16-SEP-2004.
PA (NNAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
Query Match 6.4%; Score 66; DB 8; Length 3084;
Best Local Similarity 26.5%; Pred. No. 1.4e+04;
RESULT 1244
ID AAB19795 standard; protein; 3106 AA.
DE Mouse laminin 2 alpha-2 chain.
PN WO200066730-A2.
PD 09-NOV-2000.
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
Query Match 6.4%; Score 66; DB 3; Length 3106;
Best Local Similarity 26.5%; Pred. No. 1.4e+04;
RESULT 1245
ID ADE61792 standard; protein; 3106 AA.
DE Rat Protein AAC52165, SEQ ID NO 7719.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.4%; Score 66; DB 7; Length 3106;
Best Local Similarity 26.5%; Pred. No. 1.4e+04;
RESULT 1246
ID AAE07007 standard; protein; 112 AA.
DE Human kappa light chain variable (VK) region, IL20.
PN WO200157226-A1.
PD 09-AUG-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 6.3%; Score 65.5; DB 4; Length 112;
Best Local Similarity 25.9%; Pred. No. 1.7e+02;

RESULT 1247
ID ADQ9292 standard; protein; 112 AA.
DE Human immunoglobulin protein #19.
FN US2004151721-A1.
PD 05-AUG-2004.
PA (OKEE/) O'KEEFE T.
PA (PONA/) PONATH P.
Query Match 6.3%; Score 65.5; DB 8; Length 112;
Best Local Similarity 25.9%; Pred. No. 1.7e+02;
RESULT 1248
ID AAY96955 standard; protein; 124 AA.
DE Beta-amylloid rubredoxin fusion protein.
FN WO200039310-A1.
PD 06-JUL-2000.
PA (UYGE-) UNIV GEORGIA RES FOUND INC.
Query Match 6.3%; Score 65.5; DB 3; Length 124;
Best Local Similarity 25.6%; Pred. No. 1.9e+02;
RESULT 1249
ID AAO2509 standard; protein; 131 AA.
DE Human polypeptide SEQ ID NO 16401.
FN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.3%; Score 65.5; DB 4; Length 131;
Best Local Similarity 21.3%; Pred. No. 2.1e+02;
RESULT 1250
ID AAU4892 standard; protein; 197 AA.
DE Propionibacterium acnes immunogenic protein #9878.
FN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 6.3%; Score 65.5; DB 4; Length 197;
Best Local Similarity 26.5%; Pred. No. 3.6e+02;
RESULT 1251
ID ABM45501 standard; protein; 197 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #10177.
FN WO200303315-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 6.3%; Score 65.5; DB 6; Length 197;
Best Local Similarity 26.5%; Pred. No. 3.6e+02;
RESULT 1252
ID ABG21950 standard; protein; 216 AA.
DE Novel human diagnostic protein #21941.
FN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.3%; Score 65.5; DB 4; Length 216;
Best Local Similarity 29.3%; Pred. No. 4.1e+02;
RESULT 1253
ID ABU23141 standard; protein; 218 AA.
DE Protein encoded by Prokaryotic essential gene #8668.
FN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.3%; Score 65.5; DB 6; Length 218;
Best Local Similarity 25.0%; Pred. No. 4.2e+02;
RESULT 1254
ID AAG91580 standard; protein; 221 AA.
DE C glutamicum protein fragment SEQ ID NO: 5334.
FN EP1108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 6.3%; Score 65.5; DB 4; Length 221;
Best Local Similarity 33.8%; Pred. No. 4.2e+02;
RESULT 1255
ID ADP76158 standard; protein; 235 AA.
DE Alfalfa STZ orthologue kruppel-like zinc finger protein, SEQ ID NO:15.
FN WO2004058980-A2.
PD 15-JUL-2004.
PA (CROP-) CROPDESIGN NV.
Query Match 6.3%; Score 65.5; DB 8; Length 235;
Best Local Similarity 22.7%; Pred. No. 4.6e+02;

RESULT 1256
ID AAY69003 standard; protein; 254 AA.
DE Amino acid sequence of a single chain anti-delta9-desaturase antibody.
FN WO200005391-A1.
PD 03-FEB-2000.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 6.3%; Score 65.5; DB 3; Length 254;
Best Local Similarity 23.4%; Pred. No. 5.1e+02;
RESULT 1257
ID ADH52865 standard; protein; 257 AA.
DE Porphyromonas cangingivalis B98 Fima protein.
FN WO2003054755-A2.
PD 03-JUL-2003.
PA (PFIZ) PFIZER PROD INC.
Query Match 6.3%; Score 65.5; DB 7; Length 257;
Best Local Similarity 27.1%; Pred. No. 5.2e+02;
RESULT 1258
ID AAM38702 standard; protein; 260 AA.
DE Human polypeptide SEQ ID NO 1847.
FN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.3%; Score 65.5; DB 4; Length 260;
Best Local Similarity 22.0%; Pred. No. 5.3e+02;
RESULT 1259
ID AAY68995 standard; protein; 271 AA.
DE Amino acid sequence of heavy chain of anti-delta9-desaturase antibody.
FN WO200005391-A1.
PD 03-FEB-2000.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 6.3%; Score 65.5; DB 3; Length 271;
Best Local Similarity 23.4%; Pred. No. 5.6e+02;
RESULT 1260
ID AAY69001 standard; protein; 271 AA.
DE Amino acid sequence of light chain of anti-delta9-desaturase antibody.
FN WO200005391-A1.
PD 03-FEB-2000.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 6.3%; Score 65.5; DB 3; Length 271;
Best Local Similarity 23.4%; Pred. No. 5.6e+02;
RESULT 1261
ID AAY69002 standard; protein; 271 AA.
DE Amino acid sequence of a single chain anti-delta9-desaturase antibody.
FN WO200005391-A1.
PD 03-FEB-2000.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 6.3%; Score 65.5; DB 3; Length 271;
Best Local Similarity 23.4%; Pred. No. 5.6e+02;
RESULT 1262
ID AAY69000 standard; protein; 274 AA.
DE Hypervariable region of anti-delta9-desaturase antibody.
FN WO200005391-A1.
PD 03-FEB-2000.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 6.3%; Score 65.5; DB 3; Length 271;
Best Local Similarity 23.4%; Pred. No. 5.6e+02;
RESULT 1263
ID AAUI6123 standard; protein; 281 AA.
DE Human novel secreted protein, Seq ID 1076.
FN WO200155322-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.3%; Score 65.5; DB 4; Length 281;
Best Local Similarity 22.1%; Pred. No. 5.9e+02;
RESULT 1264
ID ABU55192 standard; protein; 281 AA.
DE Human novel polypeptide #279.
FN US2002132753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 6.3%; Score 65.5; DB 6; Length 281;

Best Local Similarity 22.1%; Pred. No. 5.9e+02;
RESULT 1265
ID ADH2861 standard; protein; 281 AA.
DE Porphyromonas gulae B43 Fima protein.
PN WO2003054755-A2.
PD 03-JUL-2003.
PA (PFIZ) PRIZER PROD INC.
Query Match 6.3%; Score 65.5; DB 7; Length 281;
Best Local Similarity 27.1%; Pred. No. 5.9e+02;
RESULT 1266
ID ABM81751 standard; protein; 309 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO82592, SEQ:4515.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 65.5; DB 8; Length 309;
Best Local Similarity 21.9%; Pred. No. 6.7e+02;
RESULT 1267
ID ABR39105 standard; protein; 312 AA.
DE Human protein 34.32 SEQ ID NO:2.
PN CN1376886-A.
PD 30-OCT-2002.
PA (BIOW-) BOWINDOW GENE DEV INC SHANGHAI.
Query Match 6.3%; Score 65.5; DB 6; Length 312;
Best Local Similarity 23.6%; Pred. No. 6.8e+02;
RESULT 1268
ID ADE1283 standard; protein; 315 AA.
DE Novel human protein #37.
PN JP2002345493-A.
PD 03-DEC-2002.
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
Query Match 6.3%; Score 65.5; DB 7; Length 315;
Best Local Similarity 23.6%; Pred. No. 6.9e+02;
RESULT 1269
ID ADC37449 standard; protein; 358 AA.
DE Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 282.
PN WO2003048202-A2.
PD 12-JUN-2003.
PA (ASAH) ASAH KASEI KK.
Query Match 6.3%; Score 65.5; DB 7; Length 358;
Best Local Similarity 27.8%; Pred. No. 8.2e+02;
RESULT 1270
ID AAY13569 standard; protein; 370 AA.
DE Comm polypeptide.
PN WO925833-A1.
PD 27-MAY-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 6.3%; Score 65.5; DB 2; Length 370;
Best Local Similarity 20.5%; Pred. No. 8.6e+02;
RESULT 1271
ID ABB6658 standard; protein; 370 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 26466.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.3%; Score 65.5; DB 4; Length 370;
Best Local Similarity 20.5%; Pred. No. 8.6e+02;
RESULT 1272
ID AAM40488 standard; protein; 378 AA.
DE Human polypeptide SEQ ID NO 5419.
PN WO200153112-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.3%; Score 65.5; DB 4; Length 378;
Best Local Similarity 22.0%; Pred. No. 8.8e+02;
RESULT 1273
ID ABG08407 standard; protein; 380 AA.
DE Novel human diagnostic protein #8398.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.3%; Score 65.5; DB 4; Length 380;
Best Local Similarity 22.8%; Pred. No. 8.9e+02;

RESULT 1274
ID ABG07024 standard; protein; 380 AA.
DE Novel human diagnostic protein #7015.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.3%; Score 65.5; DB 4; Length 380;
Best Local Similarity 22.8%; Pred. No. 8.9e+02;
RESULT 1275
ID AAM41066 standard; protein; 423 AA.
DE BVDV-II gp53 polypeptide.
PN US5709865-A.
PD 20-JAN-1998.
PA (BIOS-) BIOSSTAR INC.
Query Match 6.3%; Score 65.5; DB 2; Length 423;
Best Local Similarity 24.2%; Pred. No. 1e+03;
RESULT 1276
ID AAY78891 standard; protein; 423 AA.
DE BVDVII glycoprotein 53 fragment amino acid sequence.
PN US6015795-A.
PD 18-JAN-2000.
PA (BIOS-) BIOSSTAR INC.
Query Match 6.3%; Score 65.5; DB 3; Length 423;
Best Local Similarity 24.2%; Pred. No. 1e+03;
RESULT 1277
ID ADC37447 standard; protein; 513 AA.
DE Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 280.
PN WO2003048202-A2.
PD 12-JUN-2003.
PA (ASAH) ASAH KASEI KK.
Query Match 6.3%; Score 65.5; DB 7; Length 513;
Best Local Similarity 27.8%; Pred. No. 1.3e+03;
RESULT 1278
ID ADS88185 standard; protein; 513 AA.
DE Human protein of a TNF-alpha signalling pathway protein complex SeqID 40.
PN WO2004035783-A2.
PD 29-APR-2004.
PA (CELL-) CELLZOME AG.
Query Match 6.3%; Score 65.5; DB 8; Length 513;
Best Local Similarity 27.8%; Pred. No. 1.3e+03;
RESULT 1279
ID ADP24478 standard; protein; 513 AA.
DE PRO polypeptide SEQ ID NO:1656.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 65.5; DB 8; Length 513;
Best Local Similarity 27.8%; Pred. No. 1.3e+03;
RESULT 1280
ID AAB43498 standard; protein; 580 AA.
DE Human cancer associated protein sequence SEQ ID NO:943.
PN WO200055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.3%; Score 65.5; DB 3; Length 580;
Best Local Similarity 27.8%; Pred. No. 1.6e+03;
RESULT 1281
ID ADN26061 standard; protein; 604 AA.
DE Bacterial polypeptide #8714.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.3%; Score 65.5; DB 8; Length 604;
Best Local Similarity 25.9%; Pred. No. 1.7e+03;
RESULT 1282
ID ABB76668 standard; protein; 612 AA.
DE New zinc finger protein.
PN CN1293252-A.
PD 02-MAY-2001.

PA (SHEN-) SHENGYUAN GENE DEV CO LTD SHANGHAI.
Query Match 6.3%; Score 65.5; DB 4; Length 612;
Best Local Similarity 24.2%; Pred. No. 1.7e+03;
RESULT 1283
ID AAB35704 standard; protein; 649 AA.
DE Pectate lyase protein sequence.
PN JP2000253888-A.
PD 19-SEP-2000.
PA (KAOS-) KAO CORP.
Query Match 6.3%; Score 65.5; DB 3; Length 649;
Best Local Similarity 22.8%; Pred. No. 1.8e+03;
RESULT 1284
ID ABUS3239 standard; protein; 656 AA.
DE Human testes-derived protein from DKFZphtes3_4f17.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 6.3%; Score 65.5; DB 4; Length 656;
Best Local Similarity 22.0%; Pred. No. 1.9e+03;
RESULT 1285
ID ADI28417 standard; protein; 656 AA.
DE Human nuclear hormone receptor LBDG7.
PN WO2004003010-A2.
PD 08-JAN-2004.
PA (INPH-) INPHARMATICA LTD.
Query Match 6.3%; Score 65.5; DB 8; Length 656;
Best Local Similarity 22.0%; Pred. No. 1.9e+03;
RESULT 1286
ID ADN22683 standard; protein; 662 AA.
DE Bacterial polypeptide #5336.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.3%; Score 65.5; DB 8; Length 662;
Best Local Similarity 27.3%; Pred. No. 1.9e+03;
RESULT 1287
ID ADN99509 standard; protein; 664 AA.
DE Novel human protein sequence #325.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 6.3%; Score 65.5; DB 8; Length 664;
Best Local Similarity 25.4%; Pred. No. 1.9e+03;
RESULT 1288
ID ABO84707 standard; protein; 705 AA.
DE Mouse cancer-associated protein MP21-032.1.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 6.3%; Score 65.5; DB 8; Length 705;
Best Local Similarity 19.7%; Pred. No. 2.1e+03;
RESULT 1289
ID ADP49891 standard; protein; 705 AA.
DE Murine FBLN1 SEQ ID NO:98.
PN WO2004083241-A2.
PD 30-SEP-2004.
PA (TAKA-) TAKEDA CHEM IND LTD.
Query Match 6.3%; Score 65.5; DB 8; Length 705;
Best Local Similarity 19.7%; Pred. No. 2.1e+03;
RESULT 1290
ID AAB36463 standard; protein; 726 AA.
DE Human plakophilin ppla (PKP1a) protein SEQ ID NO:3.
PN WO200066619-A2.
PD 09-NOV-2000.
PA (VLAA-) VLAAHS INTERUNIVERSITAIR INST BIOTECHNOG.
Query Match 6.3%; Score 65.5; DB 3; Length 726;
Best Local Similarity 27.6%; Pred. No. 2.2e+03;
RESULT 1291
ID ABUS6444 standard; protein; 726 AA.

DE Lung cancer-associated polypeptide #37.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (BOSB-) BOS BIOTECHNOLOGY INC.
Query Match 6.3%; Score 65.5; DB 6; Length 726;
Best Local Similarity 27.6%; Pred. No. 2.2e+03;
RESULT 1292
ID ADN04174 standard; protein; 726 AA.
DE Antipsoriatic protein sequence #282.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match 6.3%; Score 65.5; DB 8; Length 726;
Best Local Similarity 27.6%; Pred. No. 2.2e+03;
RESULT 1293
ID ABB52870 standard; protein; 744 AA.
DE Escherichia coli polypeptide SEQ ID NO 1149.
PN WO200166572-A2.
PD 13-SEP-2001.
PA (INRM-) INSERM INST NAT SANTE & RECH MEDICALE.
Query Match 6.3%; Score 65.5; DB 4; Length 744;
Best Local Similarity 34.5%; Pred. No. 2.2e+03;
RESULT 1294
ID ADH09487 standard; protein; 751 AA.
DE Human host factor protein, SEQ ID NO 15.
PN WO2003094847-A2.
PD 20-NOV-2003.
PA (UYEM-) UNIV EMORY.
Query Match 6.3%; Score 65.5; DB 8; Length 751;
Best Local Similarity 32.6%; Pred. No. 2.3e+03;
RESULT 1295
ID ABG21360 standard; protein; 806 AA.
DE Novel human diagnostic protein #21351.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.3%; Score 65.5; DB 4; Length 806;
Best Local Similarity 27.8%; Pred. No. 2.5e+03;
RESULT 1296
ID ABB60368 standard; protein; 817 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 7896.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 6.3%; Score 65.5; DB 4; Length 817;
Best Local Similarity 26.8%; Pred. No. 2.5e+03;
RESULT 1297
ID ABG91016 standard; protein; 876 AA.
DE Breast specific polypeptide #45.
PN WO200264741-A2.
PD 22-AUG-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 6.3%; Score 65.5; DB 5; Length 876;
Best Local Similarity 21.4%; Pred. No. 2.8e+03;
RESULT 1298
ID ABR41643 standard; protein; 876 AA.
DE Human DITRP cytoskeletal protein.
PN WO200297031-A2.
PD 05-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.3%; Score 65.5; DB 6; Length 876;
Best Local Similarity 21.4%; Pred. No. 2.8e+03;
RESULT 1299
ID ADN21552 standard; protein; 903 AA.
DE Bacterial polypeptide #4205.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.3%; Score 65.5; DB 8; Length 903;

Best Local Similarity 26.7%; Pred. No. 2.9e+03;
RESULT 1300
ID AAG82343 standard; protein; 1155 AA.
DE S. epidermidis open reading frame protein sequence SEQ ID NO:1780.
PN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAXO) GLAXO GROUP LTD.
Query Match 6.3%; Score 65.5; DB 4; Length 1155;
Best Local Similarity 22.6%; Pred. No. 4.1e+03;
RESULT 1301
ID ABB57176 standard; protein; 1378 AA.
DE Mouse ischaemic condition related protein sequence SEQ ID NO:428.
PN WO200188188-A2.
PD 22-NOV-2001.
PA (UNIV-) UNIV NIHON SCHOOL JURIDICAL PERSON.
Query Match 6.3%; Score 65.5; DB 5; Length 1378;
Best Local Similarity 19.3%; Pred. No. 5.2e+03;
RESULT 1302
ID ABB65499 standard; protein; 1416 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 23289.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.3%; Score 65.5; DB 4; Length 1416;
Best Local Similarity 21.8%; Pred. No. 5.4e+03;
RESULT 1303
ID AAE18208 standard; protein; 1473 AA.
DE Human MOL1b protein.
PN WO200206339-A2.
PD 24-JAN-2002.
PA (CURA-) CURAGEN CORP.
Query Match 6.3%; Score 65.5; DB 5; Length 1473;
Best Local Similarity 23.6%; Pred. No. 5.7e+03;
RESULT 1304
ID ADD18194 standard; protein; 1473 AA.
DE Human molecule (MOL) protein MOL1b.
PN WO2003003984-A2.
PD 16-JAN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.3%; Score 65.5; DB 7; Length 1473;
Best Local Similarity 23.6%; Pred. No. 5.7e+03;
RESULT 1305
ID ABG18797 standard; protein; 1494 AA.
DE Novel human diagnostic protein #18788.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.3%; Score 65.5; DB 4; Length 1484;
Best Local Similarity 23.6%; Pred. No. 5.7e+03;
RESULT 1306
ID ADS10548 standard; protein; 1693 AA.
DE Human therapeutic protein - SEQ ID 785.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 6.3%; Score 65.5; DB 8; Length 1693;
Best Local Similarity 22.4%; Pred. No. 6.9e+03;
RESULT 1307
ID ADC31103 standard; protein; 1952 AA.
DE Human novel polypeptide sequence, SEQ ID NO:1185.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 6.3%; Score 65.5; DB 7; Length 1952;
Best Local Similarity 22.4%; Pred. No. 8.4e+03;
RESULT 1308
ID ABG16404 standard; protein; 1982 AA.
DE Novel human diagnostic protein #16395.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.3%; Score 65.5; DB 4; Length 1982;
Best Local Similarity 21.9%; Pred. No. 8.5e+03;

RESULT 1309
ID ABG19656 standard; protein; 1982 AA.
DE Novel human diagnostic protein #19647.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.3%; Score 65.5; DB 4; Length 1982;
Best Local Similarity 21.9%; Pred. No. 8.5e+03;
RESULT 1310
ID AD019071 standard; protein; 1983 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1890.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 6.3%; Score 65.5; DB 8; Length 1983;
Best Local Similarity 21.9%; Pred. No. 8.5e+03;
RESULT 1311
ID AAO27065 standard; protein; 2471 AA.
DE Human Notch protein homologue sequence, SEQ ID NO 19.
PN WO9407474-A1.
PD 14-APR-1994.
PA (UYVA) UNIV YALE.
Query Match 6.3%; Score 65.5; DB 2; Length 2471;
Best Local Similarity 23.6%; Pred. No. 1.2e+04;
RESULT 1312
ID AAY06816 standard; protein; 2471 AA.
DE Human Notch2 (humN2) protein sequence.
PN WO9904746-A2.
PD 04-FEB-1999.
PA (UYVA) UNIV YALE.
Query Match 6.3%; Score 65.5; DB 2; Length 2471;
Best Local Similarity 23.6%; Pred. No. 1.2e+04;
RESULT 1313
ID AAG79774 standard; protein; 2471 AA.
DE Human Notch 2.
PN WO200296952-A2.
PD 05-DEC-2002.
PA (LORA-) LORANTIS LTD.
Query Match 6.3%; Score 65.5; DB 6; Length 2471;
Best Local Similarity 23.6%; Pred. No. 1.2e+04;
RESULT 1314
ID ABP72572 standard; protein; 2471 AA.
DE Human Notch 2.
PN WO2003012441-A1.
PD 13-FEB-2003.
PA (LORA-) LORANTIS LTD.
Query Match 6.3%; Score 65.5; DB 6; Length 2471;
Best Local Similarity 23.6%; Pred. No. 1.2e+04;
RESULT 1315
ID ABR61831 standard; protein; 2471 AA.
DE Human Notch 2 protein sequence.
PN WO2003041735-A2.
PD 22-MAY-2003.
PA (LORA-) LORANTIS LTD.
Query Match 6.3%; Score 65.5; DB 6; Length 2471;
Best Local Similarity 23.6%; Pred. No. 1.2e+04;
RESULT 1316
ID ABR61760 standard; protein; 2471 AA.
DE Human Notch 2 protein sequence.
PN WO2003042246-A2.
PD 22-MAY-2003.
PA (LORA-) LORANTIS LTD.
Query Match 6.3%; Score 65.5; DB 7; Length 2471;
Best Local Similarity 23.6%; Pred. No. 1.2e+04;
RESULT 1317
ID ADE58245 standard; protein; 2471 AA.
DE Human Protein AAA36377, SEQ ID NO 4116.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GENO) GEN HOSPITAL CORP.
Query Match 6.3%; Score 65.5; DB 7; Length 2471;
Best Local Similarity 23.6%; Pred. No. 1.2e+04;

RESULT 1318
ID ADE63707 standard; protein; 2471 AA.
DE Human Protein XP_034671, SEQ ID NO 9651.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GHEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.3%; Score 65.5; DB 7; Length 2471;
Best Local Similarity 23.6%; Pred. No. 1.2e+04;
RESULT 1319
ID ADE63703 standard; protein; 2471 AA.
DE Human Protein XP_034671, SEQ ID NO 9647.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GHEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.3%; Score 65.5; DB 7; Length 2471;
Best Local Similarity 23.6%; Pred. No. 1.2e+04;
RESULT 1320
ID ADE63715 standard; protein; 2471 AA.
DE Human Protein XP_034671, SEQ ID NO 9659.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GHEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.3%; Score 65.5; DB 7; Length 2471;
Best Local Similarity 23.6%; Pred. No. 1.2e+04;
RESULT 1321
ID ADE63711 standard; protein; 2471 AA.
DE Human Protein XP_034671, SEQ ID NO 9655.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GHEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.3%; Score 65.5; DB 7; Length 2471;
Best Local Similarity 23.6%; Pred. No. 1.2e+04;
RESULT 1322
ID ADL26913 standard; protein; 2471 AA.
DE Human Notch2 (humN2) protein.
PN US6692919-B1.
PD 17-FEB-2004.
PA (UYVA) UNIV YALE.
Query Match 6.3%; Score 65.5; DB 8; Length 2471;
Best Local Similarity 23.6%; Pred. No. 1.2e+04;
RESULT 1323
ID ADM41517 standard; protein; 2471 AA.
DE Human Notch 2.
PN WO2004022730-A1.
PD 18-MAR-2004.
PA (LORA-) LORANTIS LTD.
Query Match 6.3%; Score 65.5; DB 8; Length 2471;
Best Local Similarity 23.6%; Pred. No. 1.2e+04;
RESULT 1324
ID ADP67249 standard; protein; 2471 AA.
DE Human Notch2 protein.
PN WO2004052389-A2.
PD 24-JUN-2004.
PA (SIGE-) SINGAPORE GEN HOSPITAL PTE LTD.
PA (FORR-) FORREST G R.
Query Match 6.3%; Score 65.5; DB 8; Length 2471;
Best Local Similarity 23.6%; Pred. No. 1.2e+04;
RESULT 1325
ID ABM91619 standard; protein; 2871 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PROB2435, SEQ:4185.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 65.5; DB 8; Length 2871;
Best Local Similarity 21.8%; Pred. No. 1.4e+04;
RESULT 1326
ID AAE34399 standard; protein; 3002 AA.
DE Human fibrillin-1 protein.
PN WO200295415-A2.

PD 28-NOV-2002.
PA (OSTE-) OSTEOMETER BIO TECH AS.
Query Match 6.3%; Score 65.5; DB 6; Length 3002;
Best Local Similarity 21.8%; Pred. No. 1.5e+04;
RESULT 1327
ID ABO07260 standard; protein; 3002 AA.
DE Human p53 modifying protein, SEQ ID 220.
PN WO200299122-A1.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 6.3%; Score 65.5; DB 6; Length 3002;
Best Local Similarity 21.8%; Pred. No. 1.5e+04;
RESULT 1328
ID ADJ68389 standard; protein; 3002 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID195.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 6.3%; Score 65.5; DB 7; Length 3002;
Best Local Similarity 21.8%; Pred. No. 1.5e+04;
RESULT 1329
ID ADQ17682 standard; protein; 3002 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 499.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 6.3%; Score 65.5; DB 8; Length 3002;
Best Local Similarity 21.8%; Pred. No. 1.5e+04;
RESULT 1330
ID ADN23493 standard; protein; 3672 AA.
DE Bacterial polypeptide #6146.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.3%; Score 65.5; DB 8; Length 3672;
Best Local Similarity 20.8%; Pred. No. 2e+04;
RESULT 1331
ID ADR66062 standard; protein; 5614 AA.
DE Human prostatic carcinoma derived protein SEQ ID 258 #1.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILASKY C.
Query Match 6.3%; Score 65.5; DB 8; Length 5614;
Best Local Similarity 22.4%; Pred. No. 3.5e+04;
RESULT 1332
ID ADR66404 standard; protein; 5614 AA.
DE Human prostatic carcinoma derived protein SEQ ID 258 #2.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILASKY C.
Query Match 6.3%; Score 65.5; DB 8; Length 5614;
Best Local Similarity 22.4%; Pred. No. 3.5e+04;
RESULT 1333
ID ABG74786 standard; protein; 31267 AA.
DE Human RGS11 protein.
PN WO2002103355-A1.
PD 27-DEC-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 6.3%; Score 65.5; DB 6; Length 31267;
Best Local Similarity 22.4%; Pred. No. 3.4e+05;

RESULT 1334
ID AAB80396 standard; protein; 92 AA.
DE Secreted protein encoded by gene #26.
PN WO200107459-A1.
PD 01-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.3%; Score 65; DB 4; Length 92;
Best Local Similarity 61.9%; Pred. No. 1.4e+02;
RESULT 1335
ID ABG65277 standard; protein; 92 AA.
DE Human albumin fusion protein #1952.
PN WO2001717137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.3%; Score 65; DB 5; Length 92;
Best Local Similarity 61.9%; Pred. No. 1.4e+02;
RESULT 1336
ID ADL78544 standard; protein; 92 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 2026.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
Query Match 6.3%; Score 65; DB 8; Length 92;
Best Local Similarity 61.9%; Pred. No. 1.4e+02;
RESULT 1337
ID ABR55808 standard; protein; 110 AA.
DE Lambda chain variable region of anti-Ang-2 antibody Fb1-A7 lambda.
PN WO2003030833-A2.
PD 17-APR-2003.
PA (AMGE-) AMGEN INC.
Query Match 6.3%; Score 65; DB 6; Length 110;
Best Local Similarity 27.6%; Pred. No. 1.8e+02;
RESULT 1338
ID ABG28201 standard; protein; 117 AA.
DE Novel human diagnostic protein #28192.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.3%; Score 65; DB 4; Length 117;
Best Local Similarity 31.8%; Pred. No. 2e+02;
RESULT 1339
ID ABR55906 standard; protein; 131 AA.
DE Human mAb 2E11 light chain VJ region.
PN WO200276406-A2.
PD 03-OCT-2002.
PA (GERS/) GERSHWIN M E.
Query Match 6.3%; Score 65; DB 6; Length 131;
Best Local Similarity 24.4%; Pred. No. 2.3e+02;
RESULT 1340
ID AAY69006 standard; protein; 148 AA.
DE Amino acid sequence of light chain of anti-delta9-desaturase antibody.
PN WO200005391-A1.
PD 03-FEB-2000.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 6.3%; Score 65; DB 3; Length 148;
Best Local Similarity 23.0%; Pred. No. 2.8e+02;
RESULT 1341
ID AAG09016 standard; protein; 149 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 6781.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.3%; Score 65; DB 3; Length 149;
Best Local Similarity 26.3%; Pred. No. 2.8e+02;
RESULT 1342
ID AAG43893 standard; protein; 149 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 54916.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.3%; Score 65; DB 3; Length 149;
Best Local Similarity 26.3%; Pred. No. 2.8e+02;
RESULT 1343
ID AAW58395 standard; protein; 193 AA.

DE Homo sapiens HLIM-1 protein.
PN WO9818822-A2.
PD 07-MAY-1998.
PA (INCY-) INCYTE PHARM INC.
Query Match 6.3%; Score 65; DB 2; Length 193;
Best Local Similarity 20.7%; Pred. No. 4e+02;
RESULT 1344
ID AAU28243 standard; protein; 200 AA.
DE Novel human secretory protein, Seq ID NO 600.
PN WO200166689-A2.
PD 13-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.3%; Score 65; DB 4; Length 200;
Best Local Similarity 18.5%; Pred. No. 4.2e+02;
RESULT 1345
ID ADP76174 standard; protein; 215 AA.
DE Arabidopsis thaliana STZ paralogue, SEQ ID NO:31.
PN WO2004058980-A2.
PD 15-JUL-2004.
PA (CROP-) CROPDESIGN NV.
Query Match 6.3%; Score 65; DB 8; Length 215;
Best Local Similarity 22.6%; Pred. No. 4.6e+02;
RESULT 1346
ID ABR39464 standard; protein; 219 AA.
DE Humanised anti-Abeta antibody 266 light chain.
PN WO2003016467-A2.
PD 27-FEB-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 6.3%; Score 65; DB 6; Length 219;
Best Local Similarity 24.4%; Pred. No. 4.7e+02;
RESULT 1347
ID ABU08310 standard; protein; 219 AA.
DE Humanised 266 antibody light chain.
PN WO2003015691-A2.
PD 27-FEB-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 6.3%; Score 65; DB 6; Length 219;
Best Local Similarity 24.4%; Pred. No. 4.7e+02;
RESULT 1348
ID ABR39792 standard; peptide; 219 AA.
DE Humanised anti-Abeta antibody 266 light chain.
PN WO2003016466-A2.
PD 27-FEB-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 6.3%; Score 65; DB 6; Length 219;
Best Local Similarity 24.4%; Pred. No. 4.7e+02;
RESULT 1349
ID ABB80108 standard; protein; 219 AA.
DE Light chain.
PN WO2003015617-A2.
PD 27-FEB-2003.
PA (UNIW) UNIV WASHINGTON.
Query Match 6.3%; Score 65; DB 6; Length 219;
Best Local Similarity 24.4%; Pred. No. 4.7e+02;
RESULT 1350
ID ADE94065 standard; protein; 219 AA.
DE Humanised anti-Abeta antibody 266 light chain SEQ ID NO:11.
PN WO2003090772-A1.
PD 06-NOV-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 6.3%; Score 65; DB 7; Length 219;
Best Local Similarity 24.4%; Pred. No. 4.7e+02;
RESULT 1351
ID ADN61713 standard; protein; 219 AA.
DE Humanised antibody light chain variable region #3.
PN US2004043418-A1.
PD 04-MAR-2004.
PA (HOLT/) HOLTZMAN D M.
PA (DEMA/) DEMATOS R.
PA (BALE/) BALES K R.
PA (PAUL/) PAUL S M.
PA (TSUR/) TSURUSHITA N.

PA (VASQ/) VASQUEZ M. 6.3%; Score 65; DB 8; Length 219;
Query Match 24.4%; Pred. No. 4.7e+02;
Best Local Similarity 24.4%; Pred. No. 4.7e+02;
RESULT 1352
ID ADP84966 standard; protein; 219 AA.
DE Murine antibody fragment mlgM-Kar04 SEQ ID NO 108.
PN WO2004050707-A2.
PD 17-JUN-2004.
PA (NEMO-) NEMOD BIOTHERAPEUTICS GMBH & CO KG.
Query Match 6.3%; Score 65; DB 8; Length 219;
Best Local Similarity 22.9%; Pred. No. 4.7e+02;
RESULT 1353
ID AB860763 standard; protein; 223 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 9081.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY. 6.3%; Score 65; DB 4; Length 223;
Query Match 22.8%; Pred. No. 4.8e+02;
Best Local Similarity 22.8%; Pred. No. 4.8e+02;
RESULT 1354
ID AAU07744 standard; protein; 238 AA.
DE Humanised monoclonal antibody Hu266, light chain.
PN WO200162801-A2.
PD 30-AUG-2001.
PA (UNIW) UNIV WASHINGTON.
PA (ELIL) LILLY & CO ELI.
Query Match 6.3%; Score 65; DB 4; Length 238;
Best Local Similarity 24.4%; Pred. No. 5.3e+02;
RESULT 1355
ID ABR39842 standard; protein; 238 AA.
DE Humanised anti-Abeta antibody 266 light chain.
PN WO2003016466-A2.
PD 27-FEB-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 6.3%; Score 65; DB 6; Length 238;
Best Local Similarity 24.4%; Pred. No. 5.3e+02;
RESULT 1356
ID AAB79068 standard; protein; 242 AA.
DE Corynebacterium glutamicum HA protein sequence SEQ ID NO:92.
PN WO200100842-A2.
PD 04-JAN-2001.
PA (BADI) BASF AG. 6.3%; Score 65; DB 4; Length 242;
Query Match 20.8%; Pred. No. 5.4e+02;
Best Local Similarity 20.8%; Pred. No. 5.4e+02;
RESULT 1357
ID ADC95038 standard; protein; 243 AA.
DE E. faecium protein sequence SEQ ID 4665.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.3%; Score 65; DB 7; Length 243;
Best Local Similarity 21.9%; Pred. No. 5.4e+02;
RESULT 1358
ID AAW17058 standard; protein; 246 AA.
DE Cowpox virus chemokine inhibitor p35.
PN WO9711714-A1.
PD 03-APR-1997.
PA (IMMV) IMMUNEX CORP.
Query Match 6.3%; Score 65; DB 2; Length 246;
Best Local Similarity 25.7%; Pred. No. 5.5e+02;
RESULT 1359
ID AAW94242 standard; protein; 246 AA.
DE Cowpox p35 protein.
PN US5871740-A.
PD 16-FEB-1999.
PA (IMMV) IMMUNEX CORP.
Query Match 6.3%; Score 65; DB 2; Length 246;
Best Local Similarity 25.7%; Pred. No. 5.5e+02;
RESULT 1360
ID ADE79932 standard; protein; 246 AA.
DE Cowpox virus type-2 chemokine binding protein.
PN US6589933-B1.
PD 08-JUL-2003.

PA (VIRO-) VIRON THERAPEUTICS INC.
Query Match 6.3%; Score 65; DB 7; Length 246;
Best Local Similarity 25.7%; Pred. No. 5.5e+02;
RESULT 1361
ID AAB79067 standard; protein; 267 AA.
DE Corynebacterium glutamicum HA protein sequence SEQ ID NO:90.
PN WO200100842-A2.
PD 04-JAN-2001.
PA (BADI) BASF AG. 6.3%; Score 65; DB 4; Length 267;
Query Match 20.8%; Pred. No. 6.2e+02;
Best Local Similarity 20.8%; Pred. No. 6.2e+02;
RESULT 1362
ID ABM82737 standard; protein; 313 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:2986.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP. 6.3%; Score 65; DB 8; Length 313;
Query Match 17.4%; Pred. No. 7.7e+02;
Best Local Similarity 17.4%; Pred. No. 7.7e+02;
RESULT 1363
ID ADS29509 standard; protein; 323 AA.
DE Bacterial polypeptide #18542.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY) CAO Y. 6.3%; Score 65; DB 8; Length 323;
PA (HINK) HINKLE G J. 6.3%; Score 65; DB 8; Length 323;
PA (SLAT) SLATER S C. 6.3%; Score 65; DB 8; Length 323;
PA (CHEN) CHEN X. 6.3%; Score 65; DB 8; Length 323;
PA (GOLD) GOLDMAN B S. 6.3%; Score 65; DB 8; Length 323;
Query Match 21.6%; Pred. No. 8e+02;
Best Local Similarity 21.6%; Pred. No. 8e+02;
RESULT 1364
ID ADB85164 standard; protein; 359 AA.
DE Rat GM3 synthase SEQ ID NO:45.
PN EP1284297-A2.
PD 19-FEB-2003.
PA (WARN) WARNER LAMBERT CO. 6.3%; Score 65; DB 7; Length 359;
Query Match 22.7%; Pred. No. 9.3e+02;
Best Local Similarity 22.7%; Pred. No. 9.3e+02;
RESULT 1365
ID ABO58485 standard; protein; 369 AA.
DE Human genome derived single exon protein #4719.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN) PENN S G. 6.3%; Score 65; DB 4; Length 379;
PA (RANK) RANK D R. 6.3%; Score 65; DB 4; Length 379;
PA (HANZ) HANZEL D K. 6.3%; Score 65; DB 4; Length 379;
Query Match 21.4%; Pred. No. 9.6e+02;
Best Local Similarity 21.4%; Pred. No. 9.6e+02;
RESULT 1366
ID AAG90501 standard; protein; 379 AA.
DE C glutamicum protein fragment SEQ ID NO: 4255.
PN EP1108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK. 6.3%; Score 65; DB 4; Length 379;
Query Match 20.8%; Pred. No. 1e+03;
Best Local Similarity 20.8%; Pred. No. 1e+03;
RESULT 1367
ID ADC33030 standard; protein; 408 AA.
DE Human novel contig-encoded polypeptide sequence, SEQ ID NO:3112.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC. 6.3%; Score 65; DB 7; Length 408;
Query Match 22.0%; Pred. No. 1.1e+03;
Best Local Similarity 22.0%; Pred. No. 1.1e+03;
RESULT 1368
ID AAP70312 standard; protein; 430 AA.
DE Sequence encoded by prepro Rhizomucor miehei aspartic proteinase (RMP)
DE CDNA.
PN EP238023-A.
PD 23-SEP-1987.
PA (NOVO) NOVO TERAPEUTISK LAB AS. 6.3%; Score 65; DB 1; Length 430;
Query Match 6.3%; Score 65; DB 1; Length 430;

Best Local Similarity 27.1%; Pred. No. 1.2e+03;
RESULT 1369
ID AAP70224 standard; protein; 430 AA.
DE Sequence of Mucor miehei carboxyl protease.
PN EP215594-A.
PD 25-MAR-1987.
PA (GENV) GENENCOR INC.
Query Match 6.3%; Score 65; DB 1; Length 430;
Best Local Similarity 27.1%; Pred. No. 1.2e+03;
RESULT 1370
ID AAR62932 standard; protein; 430 AA.
DE Mucor miehei carboxyl protease.
PN EP625577-A1.
PD 23-NOV-1994.
PA (GENV) GENENCOR INT INC.
Query Match 6.3%; Score 65; DB 2; Length 430;
Best Local Similarity 27.1%; Pred. No. 1.2e+03;
RESULT 1371
ID ADE86694 standard; protein; 439 AA.
DE Chicken thymocyte activation and developmental protein.
PN US2003129685-A1.
PD 10-JUL-2003.
PA (NIJ/) NI J.
PA (YOUN/) YOUNG P E.
PA (KENN/) KENNY J J.
PA (OLSE/) OLSEN H S.
PA (MOOR/) MOORE P A.
PA (WEIY/) WEI Y.
PA (GREE/) GREENE J M.
PA (RUBE/) RUBEN S M.
Query Match 6.3%; Score 65; DB 8; Length 439;
Best Local Similarity 23.1%; Pred. No. 1.2e+03;
RESULT 1372
ID AAB92761 standard; protein; 441 AA.
DE Human protein sequence SEQ ID NO:11226.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 6.3%; Score 65; DB 4; Length 441;
Best Local Similarity 24.0%; Pred. No. 1.2e+03;
RESULT 1373
ID ABP43831 standard; protein; 441 AA.
DE FLJ10381 fis clone.
PN WO200231111-A2.
PD 18-APR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 6.3%; Score 65; DB 5; Length 441;
Best Local Similarity 24.0%; Pred. No. 1.2e+03;
RESULT 1374
ID ADC37576 standard; protein; 465 AA.
DE Human nucleic acid associated protein, NAAP-43.
PN WO2003046151-A2.
PD 05-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.3%; Score 65; DB 7; Length 465;
Best Local Similarity 23.2%; Pred. No. 1.3e+03;
RESULT 1375
ID AAM93961 standard; protein; 471 AA.
DE Human polypeptide, SEQ ID NO: 4169.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 6.3%; Score 65; DB 4; Length 471;
Best Local Similarity 24.6%; Pred. No. 1.3e+03;
RESULT 1376
ID ADL32136 standard; protein; 471 AA.
DE Human protein encoded by a full length cDNA clone SeqID 4169.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.3%; Score 65; DB 8; Length 471;
Best Local Similarity 24.6%; Pred. No. 1.3e+03;
RESULT 1377

ID ADN99835 standard; protein; 482 AA.
DE Novel human protein sequence #651.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 6.3%; Score 65; DB 8; Length 482;
Best Local Similarity 23.2%; Pred. No. 1.4e+03;
RESULT 1378
ID AAW12105 standard; protein; 485 AA.
DE Alpha-amyliase variant M382L.
PN WO9623873-A1.
PD 08-AUG-1996.
PA (NOVO) NOVO-NORDISK AS.
Query Match 6.3%; Score 65; DB 2; Length 485;
Best Local Similarity 28.3%; Pred. No. 1.4e+03;
RESULT 1379
ID ABB30317 standard; peptide; 492 AA.
DE Peptide #2968 encoded by breast cell single exon nucleic acid probe.
PN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.3%; Score 65; DB 4; Length 492;
Best Local Similarity 22.9%; Pred. No. 1.4e+03;
RESULT 1380
ID AAM56307 standard; protein; 492 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 28412.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.3%; Score 65; DB 4; Length 492;
Best Local Similarity 22.9%; Pred. No. 1.4e+03;
RESULT 1381
ID ADG27744 standard; protein; 499 AA.
DE Human novel protein amino acid sequence SeqID511.
PN WO200179254-A1.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.3%; Score 65; DB 4; Length 499;
Best Local Similarity 18.9%; Pred. No. 1.5e+03;
RESULT 1382
ID ABG69797 standard; protein; 504 AA.
DE Human REMAP-3 protein (incyte ID No: 7291877CD1).
PN WO200257454-A2.
PD 25-JUL-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.3%; Score 65; DB 5; Length 504;
Best Local Similarity 19.0%; Pred. No. 1.5e+03;
RESULT 1383
ID ABP62951 standard; protein; 531 AA.
DE Human polypeptide SEQ ID NO 388.
PN WO200218424-A2.
PD 07-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 6.3%; Score 65; DB 5; Length 531;
Best Local Similarity 23.6%; Pred. No. 1.6e+03;
RESULT 1384
ID ABB71953 standard; protein; 548 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 42651.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.3%; Score 65; DB 4; Length 548;
Best Local Similarity 22.8%; Pred. No. 1.7e+03;
RESULT 1385
ID ABB50230 standard; protein; 554 AA.
DE Human transcription factor TRFX-81.
PN WO200172777-A2.
PD 04-OCT-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.3%; Score 65; DB 4; Length 554;
Best Local Similarity 21.4%; Pred. No. 1.7e+03;
RESULT 1386
ID AAY28678 standard; protein; 556 AA.

DE Human cw272_7 secreted protein.
 PN WO9935165-A1.
 PD 15-JUL-1999.
 PA (GEMY) GENETICS INST INC.
 Query Match 6.3%; Score 65; DB 2; Length 556;
 Best Local Similarity 19.0%; Pred. No. 1.7e+03;
 RESULT 1387
 ID AAB39034 standard; protein; 556 AA.
 DE Human secreted protein cw272_7.
 PN WO200175068-A2.
 PD 11-OCT-2001.
 PA (GEMY) GENETICS INST INC.
 Query Match 6.3%; Score 65; DB 4; Length 556;
 Best Local Similarity 19.0%; Pred. No. 1.7e+03;
 RESULT 1388
 ID ABB55743 standard; protein; 556 AA.
 DE Human polypeptide SEQ ID NO 92.
 PN US2001039335-A1.
 PD 08-NOV-2001.
 PA (TACO/) JACOBS K.
 PA (MCCO/) MCCOY J M.
 PA (LAVA/) LAVALLIE E R.
 PA (COLL/) COLLINS-RACIE L A.
 PA (EVAN/) EVANS C.
 PA (MERB/) MERBERG D.
 PA (TREAC/) TREACY M.
 PA (AGOS/) AGOSTINO M J.
 PA (STEI/) STEININGER R J.
 PA (GPAU/) SPAULDING V.
 PA (WONG/) WONG G G.
 PA (CLAR/) CLARK H.
 PA (FECH/) FECHTEL K.
 Query Match 6.3%; Score 65; DB 5; Length 556;
 Best Local Similarity 19.0%; Pred. No. 1.7e+03;
 RESULT 1389
 ID AAM80175 standard; protein; 576 AA.
 DE Human protein SEQ ID NO 3821.
 PN WO200157190-A2.
 PD 09-AUG-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 6.3%; Score 65; DB 4; Length 576;
 Best Local Similarity 24.7%; Pred. No. 1.8e+03;
 RESULT 1390
 ID AAM80174 standard; protein; 576 AA.
 DE Human protein SEQ ID NO 3820.
 PN WO200157190-A2.
 PD 09-AUG-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 6.3%; Score 65; DB 4; Length 576;
 Best Local Similarity 24.7%; Pred. No. 1.8e+03;
 RESULT 1391
 ID AAM41932 standard; protein; 576 AA.
 DE Human polypeptide SEQ ID NO 6863.
 PN WO200153312-A1.
 PD 26-JUL-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 6.3%; Score 65; DB 4; Length 576;
 Best Local Similarity 24.7%; Pred. No. 1.8e+03;
 RESULT 1392
 ID ABB79073 standard; protein; 581 AA.
 DE Human zinc finger protein 64 SEQ ID NO:2.
 PN CN1292384-A.
 PD 25-APR-2001.
 PA (SHAN-) SHANGHAI BODAO GENE TECHNOLOGY CO LTD.
 Query Match 6.3%; Score 65; DB 4; Length 581;
 Best Local Similarity 22.9%; Pred. No. 1.8e+03;
 RESULT 1393
 ID ABB50170 standard; protein; 581 AA.
 DE Human transcription factor TRFX-21.
 PN WO200172777-A2.
 PD 04-OCT-2001.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 6.3%; Score 65; DB 4; Length 581;
 Best Local Similarity 34.2%; Pred. No. 2.3e+03;
 RESULT 1394
 ID AAR75648 standard; protein; 582 AA.
 DE Human placenta derived metalloprotease.
 PN WO9515374-A1.
 PD 08-JUN-1995.
 PA (FUJY) FUJI YAKUHI KOGYO KK.
 Query Match 6.3%; Score 65; DB 2; Length 582;
 Best Local Similarity 25.0%; Pred. No. 1.8e+03;
 RESULT 1395
 ID ADN99687 standard; protein; 588 AA.
 DE Novel human protein sequence #503.
 PN WO2004038003-A2.
 PD 06-MAY-2004.
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 Query Match 6.3%; Score 65; DB 8; Length 588;
 Best Local Similarity 21.4%; Pred. No. 1.8e+03;
 RESULT 1396
 ID ADN99685 standard; protein; 588 AA.
 DE Novel human protein sequence #501.
 PN WO2004038003-A2.
 PD 06-MAY-2004.
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 Query Match 6.3%; Score 65; DB 8; Length 588;
 Best Local Similarity 21.4%; Pred. No. 1.8e+03;
 RESULT 1397
 ID AAM79191 standard; protein; 603 AA.
 DE Human protein SEQ ID NO 1853.
 PN WO200157190-A2.
 PD 09-AUG-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 6.3%; Score 65; DB 4; Length 603;
 Best Local Similarity 24.7%; Pred. No. 1.9e+03;
 RESULT 1398
 ID AAM49530 standard; protein; 614 AA.
 DE D. japonica telomere cleaving associated protein SEQ ID NO 52.
 PN WO200188149-A1.
 PD 22-NOV-2001.
 PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
 Query Match 6.3%; Score 65; DB 5; Length 614;
 Best Local Similarity 23.8%; Pred. No. 1.9e+03;
 RESULT 1399
 ID AAM79190 standard; protein; 650 AA.
 DE Human protein SEQ ID NO 1852.
 PN WO200157190-A2.
 PD 09-AUG-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 6.3%; Score 65; DB 4; Length 650;
 Best Local Similarity 24.7%; Pred. No. 2.1e+03;
 RESULT 1400
 ID ABG16627 standard; protein; 684 AA.
 DE Novel human diagnostic protein #16618.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 6.3%; Score 65; DB 4; Length 684;
 Best Local Similarity 22.8%; Pred. No. 2.2e+03;
 RESULT 1401
 ID AAU72885 standard; protein; 708 AA.
 DE Human aspartyl protease partial protein sequence #10.
 PN WO200183782-A2.
 PD 08-NOV-2001.
 PA (SUGE-) SUGEN INC.
 Query Match 6.3%; Score 65; DB 5; Length 708;
 Best Local Similarity 34.2%; Pred. No. 2.3e+03;
 RESULT 1402
 ID AAB19179 standard; protein; 708 AA.
 DE Human protease, PRPS-16 protein.
 PN WO200208396-A2.
 PD 31-JAN-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 6.3%; Score 65; DB 5; Length 708;
 Best Local Similarity 34.2%; Pred. No. 2.3e+03;

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RESULT 1403
ID ADK37010 standard; protein; 708 AA.
DE Novel human polypeptide SeqID9092.
PN WO200216439-A2.
PD 28-FEB-2002.
PA (HYSE-) HYSEQ INC.
Query Match 6.3%; Score 65; DB 5; Length 708;
Best Local Similarity 27.9%; Pred. No. 2.3e+03;
RESULT 1404
ID AAW35315 standard; protein; 709 AA.
DE M. catarhalis Q8 transferrin binding protein tbpB.
PN WO9732980-A1.
PD 12-SEP-1997.
PA (CONN-) CONNAUGHT LAB LTD.
Query Match 6.3%; Score 65; DB 2; Length 709;
Best Local Similarity 20.4%; Pred. No. 2.4e+03;
RESULT 1405
ID ABU29831 standard; protein; 710 AA.
DE Protein encoded by Prokaryotic essential gene #15358.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.3%; Score 65; DB 6; Length 710;
Best Local Similarity 21.9%; Pred. No. 2.4e+03;
RESULT 1406
ID ADJ34788 standard; protein; 711 AA.
DE Xylanase from an environmental sample seq id 4.
PN WO2003106654-A2.
PD 24-DEC-2003.
PA (DIVE-) DIVERSA CORP.
Query Match 6.3%; Score 65; DB 8; Length 711;
Best Local Similarity 26.3%; Pred. No. 2.4e+03;
RESULT 1407
ID AAY78918 standard; protein; 721 AA.
DE Granulocytic ehrlichia BOV protein sequence.
PN WO200006744-A1.
PD 10-FEB-2000.
PA (AQU-) AQUILA BIOPHARMACEUTICALS INC.
Query Match 6.3%; Score 65; DB 3; Length 721;
Best Local Similarity 27.2%; Pred. No. 2.4e+03;
RESULT 1408
ID AAY92453 standard; protein; 762 AA.
DE GPIIb variant Cys6374Tyr.
PN WO200020634-A1.
PD 13-APR-2000.
PA (NOVA-) NOVA MOLECULAR INC.
Query Match 6.3%; Score 65; DB 3; Length 762;
Best Local Similarity 22.8%; Pred. No. 2.6e+03;
RESULT 1409
ID AAM80101 standard; protein; 774 AA.
DE Human protein seq ID NO 3747.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.3%; Score 65; DB 4; Length 774;
Best Local Similarity 22.9%; Pred. No. 2.7e+03;
RESULT 1410
ID ADR86253 standard; protein; 788 AA.
DE Aspergillus fumigatus essential gene protein #303.
PN WO2004067709-A2.
PD 12-AUG-2004.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.3%; Score 65; DB 8; Length 788;
Best Local Similarity 24.8%; Pred. No. 2.7e+03;
RESULT 1411
ID ADN06034 standard; protein; 803 AA.
DE Antipeoriatic protein sequence #1173.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match 6.3%; Score 65; DB 8; Length 803;
Best Local Similarity 23.1%; Pred. No. 2.8e+03;
RESULT 1412
ID AAM38689 standard; protein; 809 AA.
DE Human polypeptide SEQ ID NO 1834.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.3%; Score 65; DB 4; Length 809;
Best Local Similarity 23.1%; Pred. No. 2.8e+03;
RESULT 1413
ID ABU50164 standard; protein; 851 AA.
DE Protein encoded by Prokaryotic essential gene #35691.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.3%; Score 65; DB 6; Length 851;
Best Local Similarity 26.3%; Pred. No. 3e+03;
RESULT 1414
ID AAM79117 standard; protein; 868 AA.
DE Human protein SEQ ID NO 1779.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.3%; Score 65; DB 4; Length 868;
Best Local Similarity 22.9%; Pred. No. 3.1e+03;
RESULT 1415
ID AAE29932 standard; protein; 939 AA.
DE Human LP283 splice variant protein, LP345.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIT-) LILLY & CO ELI.
Query Match 6.3%; Score 65; DB 6; Length 939;
Best Local Similarity 21.2%; Pred. No. 3.5e+03;
RESULT 1416
ID ADC06801 standard; protein; 959 AA.
DE Prostate cancer-related protein unnamed 3.
PN WO2003064599-A2.
PD 07-AUG-2003.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match 6.3%; Score 65; DB 7; Length 959;
Best Local Similarity 22.3%; Pred. No. 3.6e+03;
RESULT 1417
ID AAE17967 standard; protein; 1005 AA.
DE Human Sal2 protein mutant (S73C).
PN WO200204596-A2.
PD 17-JAN-2002.
PA (HARD) HARVARD COLLEGE.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Query Match 6.3%; Score 65; DB 5; Length 1005;
Best Local Similarity 22.3%; Pred. No. 3.8e+03;
RESULT 1418
ID AAE17968 standard; protein; 1005 AA.
DE Human Sal2 protein mutant (G744R).
PN WO200204596-A2.
PD 17-JAN-2002.
PA (HARD) HARVARD COLLEGE.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Query Match 6.3%; Score 65; DB 5; Length 1005;
Best Local Similarity 22.3%; Pred. No. 3.8e+03;
RESULT 1419
ID AAE17954 standard; protein; 1005 AA.
DE Human Sal2 protein.
PN WO200204596-A2.
PD 17-JAN-2002.
PA (HARD) HARVARD COLLEGE.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Query Match 6.3%; Score 65; DB 5; Length 1005;
Best Local Similarity 22.3%; Pred. No. 3.8e+03;
RESULT 1420
ID ADC06837 standard; protein; 1005 AA.
DE Human prostate cancer-related protein PCP0815A.
PN WO2003064599-A2.
PD 07-AUG-2003.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
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Query Match 6.3%; Score 65; DB 7; Length 1005;
Best Local Similarity 22.3%; Pred. No. 3.8e+03;
RESULT 1421
ID AAM78838 standard; protein; 1007 AA.
DE Human protein SEQ ID NO 1500.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.3%; Score 65; DB 4; Length 1007;
Best Local Similarity 22.3%; Pred. No. 3.8e+03;
RESULT 1422
ID ABP96241 standard; protein; 1007 AA.
DE Human nucleic-acid associated protein 24 SEQ ID NO:24.
PN WO2003016549-A2.
PD 27-FEB-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.3%; Score 65; DB 6; Length 1007;
Best Local Similarity 22.3%; Pred. No. 3.8e+03;
RESULT 1423
ID ADC06800 standard; protein; 1007 AA.
DE Human prostate cancer-related protein XM_033473.
PN WO2003064599-A2.
PD 07-AUG-2003.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match 6.3%; Score 65; DB 7; Length 1007;
Best Local Similarity 22.3%; Pred. No. 3.8e+03;
RESULT 1424
ID ADC06835 standard; protein; 1007 AA.
DE Human prostate cancer-related protein XM_033473.
PN WO2003064599-A2.
PD 07-AUG-2003.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match 6.3%; Score 65; DB 7; Length 1007;
Best Local Similarity 22.3%; Pred. No. 3.8e+03;
RESULT 1425
ID AAM79822 standard; protein; 1019 AA.
DE Human protein SEQ ID NO 3468.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.3%; Score 65; DB 4; Length 1019;
Best Local Similarity 22.3%; Pred. No. 3.9e+03;
RESULT 1426
ID ADC06799 standard; protein; 1041 AA.
DE Human prostate cancer-related protein PCP0815.
PN WO2003064599-A2.
PD 07-AUG-2003.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match 6.3%; Score 65; DB 7; Length 1041;
Best Local Similarity 22.3%; Pred. No. 4e+03;
RESULT 1427
ID ADE95476 standard; protein; 1131 AA.
DE Human NOVX2b protein.
PN WO2003050245-A2.
PD 19-JUN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.3%; Score 65; DB 7; Length 1131;
Best Local Similarity 24.7%; Pred. No. 4.5e+03;
RESULT 1428
ID ADE95480 standard; protein; 1145 AA.
DE Human NOVX2d protein.
PN WO2003050245-A2.
PD 19-JUN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.3%; Score 65; DB 7; Length 1145;
Best Local Similarity 24.7%; Pred. No. 4.5e+03;
RESULT 1429
ID ADE95474 standard; protein; 1184 AA.
DE Human NOVX2a protein.
PN WO2003050245-A2.
PD 19-JUN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.3%; Score 65; DB 7; Length 1184;

Best Local Similarity 24.7%; Pred. No. 4.7e+03;
RESULT 1430
ID ABP63045 standard; protein; 1231 AA.
DE Human polypeptide SEQ ID NO 482.
PN WO200218424-A2.
PD 07-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 6.3%; Score 65; DB 5; Length 1231;
Best Local Similarity 24.7%; Pred. No. 5e+03;
RESULT 1431
ID ADR10325 standard; protein; 1662 AA.
DE Human protein useful for treating neurological disease Seq 3831.
PN EPI447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.3%; Score 65; DB 8; Length 1662;
Best Local Similarity 24.0%; Pred. No. 7.5e+03;
RESULT 1432
ID ABE71529 standard; protein; 3843 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 41379.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.3%; Score 65; DB 4; Length 3843;
Best Local Similarity 20.1%; Pred. No. 2.4e+04;
RESULT 1433
ID ABB97541 standard; protein; 4263 AA.
DE Novel human protein SEQ ID NO: 809.
PN WO200222660-A2.
PD 21-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 6.3%; Score 65; DB 5; Length 4263;
Best Local Similarity 23.7%; Pred. No. 2.7e+04;
RESULT 1434
ID ADM47281 standard; protein; 4264 AA.
DE Protocadherin FAT-like NOVX 28b protein.
PN WO2003083039-A2.
PD 09-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.3%; Score 65; DB 7; Length 4264;
Best Local Similarity 23.1%; Pred. No. 2.7e+04;
RESULT 1435
ID ADM74227 standard; protein; 4264 AA.
DE Human NOV6N protein sequence SeqID66.
PN WO2004015079-A2.
PD 19-FEB-2004.
PA (CURA-) CURAGEN CORP.
Query Match 6.3%; Score 65; DB 8; Length 4264;
Best Local Similarity 23.1%; Pred. No. 2.7e+04;
RESULT 1436
ID ADP04603 standard; protein; 76 AA.
DE Sea squirt protein with tissue specific expression in development Seq198.
PN JP2004057129-A.
PD 26-FEB-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 6.2%; Score 64.5; DB 8; Length 76;
Best Local Similarity 22.8%; Pred. No. 1.2e+02;
RESULT 1437
ID AAB64520 standard; protein; 101 AA.
DE Human secreted protein sequence encoded by gene 30 SRQ ID NO:158.
PN WO200077255-A1.
PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.2%; Score 64.5; DB 4; Length 101;
Best Local Similarity 26.5%; Pred. No. 1.8e+02;
RESULT 1438
ID ADL93510 standard; protein; 112 AA.
DE Human CD44-binding antibody F2 light chain variable region SEQ ID NO:5.
PN WO2004024750-A2.
PD 25-MAR-2004.
PA (DYAX-) DYAX CORP.
Query Match 6.2%; Score 64.5; DB 8; Length 112;
Best Local Similarity 28.4%; Pred. No. 2.1e+02;

RESULT 1439
ID AAG00935 standard; protein; 114 AA.
DE Human secreted protein, SEQ ID NO: 5016.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 6.2%; Score 64.5; DB 3; Length 114;
Best Local Similarity 26.5%; Pred. No. 2.2e+02;
RESULT 1440
ID AAR39711 standard; protein; 177 AA.
DE A. oryzae WT neutral protease.
PN JP05168479-A.
PD 02-JUL-1993.
PA (SHSA) SHOKUHIN SANGYO KOSOKINO HENKA.
Query Match 6.2%; Score 64.5; DB 2; Length 177;
Best Local Similarity 22.6%; Pred. No. 4e+02;
RESULT 1441
ID AAR39712 standard; protein; 177 AA.
DE A. oryzae CSA neutral protease.
PN JP05168479-A.
PD 02-JUL-1993.
PA (SHSA) SHOKUHIN SANGYO KOSOKINO HENKA.
Query Match 6.2%; Score 64.5; DB 2; Length 177;
Best Local Similarity 22.6%; Pred. No. 4e+02;
RESULT 1442
ID ABU06494 standard; protein; 212 AA.
DE Maize SSI glycosyl transferase domain (GLYTR) related protein #13.
PN WO200279410-A2.
PD 10-OCT-2002.
PA (BADI) BASF PLANT SCI GMBH.
Query Match 6.2%; Score 64.5; DB 6; Length 212;
Best Local Similarity 22.5%; Pred. No. 5.1e+02;
RESULT 1443
ID ABU06493 standard; protein; 212 AA.
DE Maize SSI glycosyl transferase domain (GLYTR) related protein #12.
PN WO200279410-A2.
PD 10-OCT-2002.
PA (BADI) BASF PLANT SCI GMBH.
Query Match 6.2%; Score 64.5; DB 6; Length 212;
Best Local Similarity 22.5%; Pred. No. 5.1e+02;
RESULT 1444
ID ABU29739 standard; protein; 215 AA.
DE Protein encoded by Prokaryotic essential gene #15266.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.2%; Score 64.5; DB 6; Length 215;
Best Local Similarity 22.0%; Pred. No. 5.2e+02;
RESULT 1445
ID AAG18166 standard; protein; 216 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 19466.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%; Score 64.5; DB 3; Length 216;
Best Local Similarity 23.0%; Pred. No. 5.2e+02;
RESULT 1446
ID AAG90867 standard; protein; 224 AA.
DE C glutamicum protein fragment SEQ ID NO: 4621.
PN EP1108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 6.2%; Score 64.5; DB 4; Length 224;
Best Local Similarity 21.9%; Pred. No. 5.5e+02;
RESULT 1447
ID APC94048 standard; protein; 231 AA.
DE E. faecium protein sequence SEQ ID 3675.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.2%; Score 64.5; DB 7; Length 231;
Best Local Similarity 22.0%; Pred. No. 5.7e+02;
RESULT 1448
ID ANG15677 standard; protein; 239 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 16025.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%; Score 64.5; DB 3; Length 239;
Best Local Similarity 22.4%; Pred. No. 6e+02;
RESULT 1449
ID AAB21017 standard; protein; 243 AA.
DE Human nucleic acid-binding protein, NuABP-21.
PN WO200044900-A2.
PD 03-AUG-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 6.2%; Score 64.5; DB 3; Length 243;
Best Local Similarity 29.6%; Pred. No. 6.1e+02;
RESULT 1450
ID ADG32321 standard; protein; 251 AA.
DE Mouse scFV VD2 antibody targeted against V_dahliae SeqID 30.
PN WO2003089475-A2.
PD 30-OCT-2003.
PA (FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.
Query Match 6.2%; Score 64.5; DB 7; Length 251;
Best Local Similarity 24.0%; Pred. No. 6.4e+02;
RESULT 1451
ID ABF45470 standard; protein; 259 AA.
DE Human Blys binding scFv SEQ ID 1481.
PN WO200202641-A1.
PD 10-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.2%; Score 64.5; DB 5; Length 259;
Best Local Similarity 19.6%; Pred. No. 6.7e+02;
RESULT 1452
ID ADG96297 standard; protein; 259 AA.
DE Single chain antibody that immunospecifically binds Blys SeqID 1481.
PN WO2003055979-A2.
PD 10-JUL-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.2%; Score 64.5; DB 7; Length 259;
Best Local Similarity 19.6%; Pred. No. 6.7e+02;
RESULT 1453
ID AAU16008 standard; protein; 261 AA.
DE Human novel secreted protein, Seq ID 961.
PN WO200155322-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.2%; Score 64.5; DB 4; Length 261;
Best Local Similarity 25.2%; Pred. No. 6.7e+02;
RESULT 1454
ID ABUS5077 standard; protein; 261 AA.
DE Human novel polypeptide #164.
PN US2002132753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 6.2%; Score 64.5; DB 6; Length 261;
Best Local Similarity 25.2%; Pred. No. 6.7e+02;
RESULT 1455
ID AAG18165 standard; protein; 265 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 19465.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%; Score 64.5; DB 3; Length 265;
Best Local Similarity 23.0%; Pred. No. 6.9e+02;
RESULT 1456
ID AAM93500 standard; protein; 269 AA.
DE Human polypeptide, SEQ ID NO: 3207.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 6.2%; Score 64.5; DB 4; Length 269;
Best Local Similarity 23.1%; Pred. No. 7e+02;
RESULT 1457
ID ADL31174 standard; protein; 269 AA.

DE Human protein encoded by a full length cDNA clone SeqID 3207.
PN EPI396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.2%; Score 64.5; DB 8; Length 269;
Best Local Similarity 23.1%; Pred. No. 7e+02;
RESULT 1458
ID ADC95316 standard; protein; 296 AA.
DE E. faecium protein sequence SEQ ID 4943.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.2%; Score 64.5; DB 7; Length 296;
Best Local Similarity 22.5%; Pred. No. 8e+02;
RESULT 1459
ID ADS24873 standard; protein; 311 AA.
DE Bacterial polypeptide #13906.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.2%; Score 64.5; DB 8; Length 311;
Best Local Similarity 24.2%; Pred. No. 8.6e+02;
RESULT 1460
ID ADC32756 standard; protein; 313 AA.
DE Human novel contig-encoded polypeptide sequence, SEQ ID NO:2838.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 6.2%; Score 64.5; DB 7; Length 313;
Best Local Similarity 24.4%; Pred. No. 8.7e+02;
RESULT 1461
ID ADG32358 standard; protein; 320 AA.
DE Precursor fusion protein of APP AG-scFV VD2 SeqID 67.
PN WO2003089475-A2.
PD 30-OCT-2003.
PA (FRAU) FRAUNHOFER GBS FOERDERUNG ANGEWANDTEN.
Query Match 6.2%; Score 64.5; DB 7; Length 320;
Best Local Similarity 24.0%; Pred. No. 8.9e+02;
RESULT 1462
ID ADO62015 standard; protein; 320 AA.
DE Transcription factor G2649, SEQ ID 482.
PN WO2004031349-A2.
PD 15-APR-2004.
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
Query Match 6.2%; Score 64.5; DB 8; Length 320;
Best Local Similarity 19.7%; Pred. No. 8.9e+02;
RESULT 1463
ID AAR14147 standard; protein; 352 AA.
DE Pre-pro neutral protease II.
PN JP03198779-A.
PD 29-AUG-1991.
PA (SHSA) SHOKUIN SANGYO KOSOKINO HENKA.
Query Match 6.2%; Score 64.5; DB 2; Length 352;
Best Local Similarity 22.6%; Pred. No. 1e+03;
RESULT 1464
ID AAY08526 standard; protein; 360 AA.
DE P. luminescens pretLuxI Lux A protein.
PN WO925866-A1.
PD 27-MAY-1999.
PA (KORP/) KORPELA M.
PA (KARP/) KARP M.
PA (KURI/) KURITTU J.
Query Match 6.2%; Score 64.5; DB 2; Length 360;
Best Local Similarity 21.4%; Pred. No. 1e+03;
RESULT 1465
ID AAR34464 standard; protein; 381 AA.
DE Bacillus amyloliquefaciens alkaline elastase.
PN WO9307276-A1.
PD 15-APR-1993.

PA (CHEM-) CHEMGEN CORP.
PA (VIST-) VISTA CHEMICAL CO.
Query Match 6.2%; Score 64.5; DB 2; Length 381;
Best Local Similarity 19.8%; Pred. No. 1.1e+03;
RESULT 1466
ID ADP04725 standard; protein; 400 AA.
DE Sea squirt protein with tissue specific expression in development Seq320.
PN JP2004057129-A.
PD 26-FEB-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 6.2%; Score 64.5; DB 8; Length 400;
Best Local Similarity 25.6%; Pred. No. 1.2e+03;
RESULT 1467
ID AAR24392 standard; protein; 402 AA.
DE Sequence of the Histidine-rich protein (HisRP) associated with the knob
DE (K+) phenotype.
PN US5116965-A.
PD 26-MAY-1992.
PA (SLOK) SLOAN KETTERING INST CANCER.
Query Match 6.2%; Score 64.5; DB 2; Length 402;
Best Local Similarity 26.1%; Pred. No. 1.2e+03;
RESULT 1468
ID ADJ48575 standard; protein; 410 AA.
DE Oil-associated gene related protein #75.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match 6.2%; Score 64.5; DB 8; Length 410;
Best Local Similarity 28.9%; Pred. No. 1.3e+03;
RESULT 1469
ID ADB65040 standard; protein; 424 AA.
DE Human protein encoded by clone SMINT20011950.
PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.2%; Score 64.5; DB 7; Length 424;
Best Local Similarity 24.4%; Pred. No. 1.3e+03;
RESULT 1470
ID AQO21269 standard; protein; 437 AA.
DE Sonic hedgehog protein mutant NS1A, VS2A, TS6A, E168A.
PN WO200224151-A2.
PD 28-MAR-2002.
PA (UVJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
Query Match 6.2%; Score 64.5; DB 5; Length 437;
Best Local Similarity 24.2%; Pred. No. 1.4e+03;
RESULT 1471
ID AAR45335 standard; protein; 461 AA.
DE Thrombomodulin analogue Q336N, Q365E.
PN WO9325675-A1.
PD 23-DEC-1993.
PA (SCHD) SCHERING AG.
Query Match 6.2%; Score 64.5; DB 2; Length 461;
Best Local Similarity 19.3%; Pred. No. 1.5e+03;
RESULT 1472
ID ABO78175 standard; protein; 472 AA.
DE Pseudomonas aeruginosa polypeptide #10350.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.2%; Score 64.5; DB 7; Length 472;
Best Local Similarity 24.3%; Pred. No. 1.5e+03;
RESULT 1473
ID AAB81188 standard; protein; 475 AA.
DE Human zinc finger protein 52 (ZFP-52).
PN WO200127151-A1.
PD 19-APR-2001.
PA (SHAN-) SHANGHAI BIO DOOR GENE TECHNOLOGY LTD.
Query Match 6.2%; Score 64.5; DB 4; Length 475;